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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:43:08 ; Search time 13.5547 Seconds
(without alignments)
538.330 Million cell updates/sec

Title: US-09-978-382A-4
Perfect score: 1263
Sequence: 1 MEEGSSHDAESSKKLGRGK.....NLLEPNQOFGSQDPPPLQLV 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCFUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1263	100.0	248	4	US-09-067-800-6
2	1263	100.0	248	4	US-09-349-677-6
3	1050	83.1	246	4	US-09-067-800-8
4	1050	83.1	246	4	US-09-349-677-8
5	806.5	63.9	248	1	US-08-460-512-7
6	770.5	61.0	226	4	US-08-433-579-2
7	769.5	60.9	241	4	US-09-410-464-12
8	752	59.5	252	1	US-08-460-512-5
9	752	59.5	285	1	US-08-460-512-2
10	751	59.5	252	1	US-08-460-512-4
11	739.5	58.6	238	4	US-09-410-464-16
12	430.5	34.1	250	2	US-08-867-087B-13
13	426	33.7	241	2	US-08-867-087B-11
14	426	33.7	273	2	US-08-592-214A-8
15	426	33.7	273	3	US-08-659-188-8
16	426	33.7	273	3	US-08-655-227-8
17	426	33.7	273	3	US-08-655-241-8
18	426	33.7	273	3	US-09-149-976-8
19	426	33.7	273	3	US-09-398-326-8
20	405.5	32.1	249	2	US-08-867-087B-15
21	402	31.8	225	2	US-08-867-087B-55
22	399.5	31.6	248	2	US-08-867-087B-17
23	397	31.4	255	2	US-08-592-214A-10
24	397	31.4	255	3	US-08-659-188-10
25	397	31.4	255	3	US-08-655-227-10
26	397	31.4	255	3	US-08-655-241-10
27	397	31.4	255	3	US-09-149-976-10

28	397	31.4	255	4	US-09-398-326-10	Sequence 10, Appl
29	392.5	31.1	251	2	US-08-592-214A-12	Sequence 12, Appl
30	392.5	31.1	251	3	US-08-659-188-12	Sequence 12, Appl
31	392.5	31.1	251	3	US-08-655-227-12	Sequence 12, Appl
32	392.5	31.1	251	3	US-08-655-241-12	Sequence 12, Appl
33	392.5	31.1	251	3	US-09-149-976-12	Sequence 12, Appl
34	392.5	31.1	251	4	US-09-398-326-12	Sequence 12, Appl
35	391	31.0	255	2	US-08-578-156-2	Sequence 2, Appl
36	391	31.0	256	3	US-08-659-188-2	Sequence 2, Appl
37	391	31.0	256	3	US-08-655-227-2	Sequence 2, Appl
38	391	31.0	256	3	US-08-655-241-2	Sequence 2, Appl
39	391	31.0	256	4	US-09-398-326-2	Sequence 2, Appl
40	391	31.0	257	2	US-08-867-087B-2	Sequence 2, Appl
41	391	31.0	300	2	US-08-592-214A-2	Sequence 2, Appl
42	391	31.0	300	3	US-09-149-976-2	Sequence 2, Appl
43	388	30.7	253	2	US-08-592-214A-4	Sequence 4, Appl
44	388	30.7	253	3	US-08-659-188-4	Sequence 4, Appl
45	388	30.7	253	3	US-08-655-227-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-067-800-6
; Sequence 6, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-067-800-6

Query Match 100.0%; Score 1263; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e-119;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEEGSSHDAESSKKLGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60
Db 1 MEEGSSHDAESSKKLGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60
QY 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPSVTEANTQYYQQEASLRRQRIDQ 120

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Db 61 VIFSTRGRLEYANNVSRGTIERYKACSDAVNPPSVTEANTQYQQEASKLRQRIDIQ 120
QY 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAETIYMQKREMELOHNNM 180
Db 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAETIYMQKREMELOHNNM 180
QY 181 YLRAKIAGARLNPDQOESSVIOGTTVYESGVSSHDSOQHYNNRNYIPVNLLEPNQOQFSQ 240
Db 181 YLRAKIAGARLNPDQOESSVIOGTTVYESGVSSHDSOQHYNNRNYIPVNLLEPNQOQFSQ 240
QY 241 DQPPLQLV 248
Db 241 DQPPLQLV 248

RESULT 2
US-09-349-677-6
; Sequence 6, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-349-677-6

Query Match 100.0%; Score 1263; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e-119;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEEGSSHDAESSKLGKRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVAL 60
Db 1 MEEGSSHDAESSKLGKRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVAL 60
QY 61 VIFSTRGRLEYANNVSRGTIERYKACSDAVNPPSVTEANTQYQQEASKLRQRIDIQ 120
Db 61 VIFSTRGRLEYANNVSRGTIERYKACSDAVNPPSVTEANTQYQQEASKLRQRIDIQ 120
QY 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAETIYMQKREMELOHNNM 180
Db 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAETIYMQKREMELOHNNM 180
QY 181 YLRAKIAGARLNPDQOESSVIOGTTVYESGVSSHDSOQHYNNRNYIPVNLLEPNQOQFSQ 240
Db 181 YLRAKIAGARLNPDQOESSVIOGTTVYESGVSSHDSOQHYNNRNYIPVNLLEPNQOQFSQ 240
QY 241 DQPPLQLV 248
Db 241 DQPPLQLV 248
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Db 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAETIYMQKREMELOHNNM 180
QY 181 YLRAKIAGARLNPDQOESSVIOGTTVYESGVSSHDSOQHYNNRNYIPVNLLEPNQOQFSQ 240
Db 181 YLRAKIAGARLNPDQOESSVIOGTTVYESGVSSHDSOQHYNNRNYIPVNLLEPNQOQFSQ 240
QY 241 DQPPLQLV 248
Db 241 DQPPLQLV 248

RESULT 3
US-09-067-800-8
; Sequence 8, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-067-800-8

Query Match 83.18; Score 1050; DB 4; Length 246;
Best Local Similarity 85.5%; Pred. No. 5.7e-98;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEEGSSHDAESSKLGKRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVAL 60
Db 1 MEEGASNEVAESSKLGKRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVAL 60
QY 61 VIFSTRGRLEYANNVSRGTIERYKACSDAVNPPSVTEANTQYQQEASKLRQRIDIQ 120
Db 61 VIFSTRGRLEYANNVSRGTIERYKACSDAVNPPSVTEANTQYQQEASKLRQRIDIQ 120
QY 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAETIYMQKREMELOHNNM 180
Db 121 NLNHHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAETIYMQKREMELOHNNM 180
QY 181 YLRAKIAGARLNPDQOESSVIOGTTVYESGVSSHDSOQHYNNRNYIPVNLLEPNQOQFSQ 240
Db 181 YLRKITE- -RTGLQQOESSVIOGTTVYESGVSSHDSOQHYNNRNYIPVNLLEPNQOQFSQ 238
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Db 123 SNRLMGETIGSMSPKELNLEGRLESIIRSKKNELLFSEIDYMKREVLDHNDNOI 182
QY 182 LRAKIAGARLNPDQOESSVIOGTTVYESGV-SSHDQSOHY-NRNYIPVNLLPEPNOQF-- 237
Db 183 LRAKIAENERNRP---SISLMPGGSNYEQLMPPPTQSQPDSRNYFQVAALQPNHHYS 272
QY 238 --SGQDPPLQLV 248
Db 240 SAGRODOTALQLV 252

RESULT 9
US-08-460-512-2
; Sequence 2, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFKY, Martin F.
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,512
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,278
; FILING DATE:
; APPLICATION NUMBER: US/07/956,694
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-512-2

Query Match 59.5%; Score 752; DB 1; Length 285;
Best Local Similarity 63.2%; Pred. No. 7.7e-68;
Matches 160; Conservative 33; Mismatches 48; Indels 12; Gaps 5;

QY 2 BEGSSHDAESSKILGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALV 61
Db 39 ELGG---DSSPLRKSGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALI 95
QY 62 IFSTRGRLYEYANNVSRGTIERYKKACSDAVNPPSVTEANTQYYQOEASKLRQIRDION 121
Db 96 VFSSRGRLYEYSNNVSGKTIERYKKAISDNTSGSVAEINAQYYQOESAKLRQIIISIQ 155
QY 122 SNRHVIGSLGSLNFKELNLEGRLEKIGTSRVRSKKNELLVAEITYMKREMELOHNNM 181
Db 156 SNRLMGETIGSMSPKELNLEGRLESIIRSKKNELLFSEIDYMKREVLDHNDNOI 215
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QY 182 LRAKIAGARLNPDQOESSVIOGTTVYESGV-SSHDQSOHY-NRNYIPVNLLPEPNOQF-- 237
Db 216 LRAKIAENERNRP---SISLMPGGSNYEQLMPPPTQSQPDSRNYFQVAALQPNHHYS 272
QY 238 --SGQDPPLQLV 248
Db 273 SAGRODOTALQLV 285

RESULT 10
US-08-460-512-4
; Sequence 4, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,512
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,278
; FILING DATE:
; APPLICATION NUMBER: US/07/956,694
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-512-4

Query Match 59.5%; Score 751; DB 1; Length 252;
Best Local Similarity 62.0%; Pred. No. 8.1e-68;
Matches 158; Conservative 34; Mismatches 49; Indels 14; Gaps 5;

QY 1 MEEGSSHDAESSKILGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVAL 60
Db 5 MELGGES---SPKAGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVAL 61
QY 61 VIFSTRGRLYEYANNVSRGTIERYKKACSDAVNPPSVTEANTQYYQOEASKLRQIRDIO 120
Db 62 IVFSSRGRLYEYSNNVSGKTIERYKKAISDNTSGSVAEINAQYYQOESAKLRQIIISQ 121
QY 121 NSNRHVIGSLGSLNFKELNLEGRLEKIGTSRVRSKKNELLVAEITYMKREMELOHNNM 180
Db 122 NSNRQLMGETIGSMSPKELNLEGRLESIIRSKKNELLFAEIDYMKREVLDHNDNQ 181
QY 181 YLRAKIAGARLNPDQOESSVIOGTTVYESGVSSHDQSOHY---NRNYIPVNLLPEPNOQF 237
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; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-867-087B-11

Query Match 33.7%; Score 426; DB 2; Length 241;
Best Local Similarity 40.4%; Pred. No. 4.3e-35;
Matches 97; Conservative 49; Mismatches 64; Indels 30; Gaps 6;

QY 16 LGRGKIEIKRIENTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYE-YAN 74
Db 1 MGRGVELKRIENKINROVTFKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYANN 75
QY 75 NSVRGTIERYKKACSDAVNPPSVT--EANTQYQOEASKLRRQIRDIONSNRHIVGESLG 132
Db 61 SSMKTLERYQK-CNYGAPETNISTREALEISSQOEYLKARYEALQRSQRLNGEDLG 119
QY 133 SLNFKELKNLEGRLEKGISRVRSKKNELLVAELEYMOKREMELOHNNMYLRAKIAEGARL 192
Db 120 PLNSKELSLERQDLSLKQINSTLTQLMDQLDQRLKEHALNEANRTLKRLMEGSQL 179
QY 193 NPDQOESSVIOGTTVYESGVSSHDSQHYNNR-----YIPVNLLEPNQOFSGQDQP 243
Db 180 NLQWQNA-----QDMGVGRTTOTQGDGFHPL-CEPTLQIGYQNDP 222

RESULT 14
US-08-592-214A-8
; Sequence 8, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
```

```
;
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-592-214A-8

Query Match 33.7%; Score 426; DB 2; Length 273;
Best Local Similarity 38.0%; Pred. No. 5.3e-35;
Matches 100; Conservative 48; Mismatches 81; Indels 34; Gaps 5;

QY 16 LGRGKIEIKRIENTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYANN 75
Db 1 MGRGVELKRIENKINROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYATD 60
QY 76 SVRGTI-----ERYKKACSDAVNPPSVTEANTQYQOEASKLRRQIRDIONSNRHIVGESL 131
Db 61 SMDKILERYERYSYAEKALISAESSEGN---WCHEYRKLKAKTETQKCHKHLMGEDL 117
QY 132 GSLNFKELKNLEGRLEKGISRVRSKKNELLVAELEYMOKREMELOHNNMYLRAKIAEGAR 191
Db 118 ESLNPKELQOEQLDSSLKHIRSRKSHLMAESISELQKRSLOEENKALQKELAEROK 177
QY 192 -----LNPDQOESSVIOGTTVYESGVSSHDSQ-----QHYNNRYIPVNL----- 230
Db 178 AVASRQOQQQQQVWDQTHAQOTSSSSSFMMRQDQGLPPPHNICFPPLTMDGRGEE 237
QY 231 -----LEPNQOFSGQDQPPLQL 247
Db 238 LAAAAAQOQQPLPGQAQPOLRI 260

RESULT 15
US-08-659-188-8
; Sequence 8, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-659-188-8
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Query Match      33.7%; Score 426; DB 3; Length 273;
Best Local Similarity 38.0%; Pred. No. 5.3e-35;
Matches 100; Conservative 48; Mismatches 81; Indels 34; Gaps 5;

QY          16 LGRGKIEIKRIENTNQVTFCKRRNGLLKKAYELSVLCDAEVALVFSTFGRGLRYEVANN 75
              : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db           1 MGRGVQLKRRIENINQVTFCKRRNGLLKKAAHEISVLCDAEVAIVFSPKGKLYEVATD 60

QY          76 SVRGTI-----ERYKKACSDAVNPSPVTEANTYYQQOEASKLRROIROIDNSNRHIVGESL 131
              : | | | : : : | : : : | : : : | : : : | : : : | : : : |
Db           61 SRMDKILERVYSYA EKALISAASEGN---WCHEYRKLUKAIETIQCKCHLMGMGDLL 117

QY          132 GSLNFKEKLNLEGRLEKGISRVSRKKNELLVAEITYMOKREMELOHNNMYLUAKIAEGAR 191
              ||| |||| : : : | : : : | : : : | : : : | : : : | : : : |
Db          118 ESLNPKELQEQQLDSLKHIRSKRHSLMAESISELQKKERSQEENKALQKELAERQK 177

QY          192 -----LNPDOGESVIQGTTVYESVGSSHQS---QHYNRMYPVNLF----- 230
              : | | | : : : | : : : | : : : | : : : | : : : | : : : |
Db          178 AVASRQOQQOQQOVWDQTHQAQTSSSSSFFMRQDOQGPPPHNICFPPLTMGDRGEE 237

QY          231 -----LEPNQQQFSGDDQPPLQL 247
              : | | | | : : : | : : : | : : : | : : : | : : : |
Db          238 LAAAAAAGCQQQQLPFGCAQPOLRI 260

```

Search completed: January 27, 2003, 12:46:49
Job time : 14.5547 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 12:42:53 ; Search time 14.5587 Seconds
(without alignments)
1637.600 Million cell updates/sec

Title: US-09-978-382A-4
Perfect score: 1263
Sequence: 1 MEEGSSHDAESSKKLGRGK.....NLLEPNQFSGDQPPLQLV 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1263	100.0	248	2 A39534	floral homeotic pr
2	1050	83.1	246	2 E39534	floral homeotic pr
3	1046	82.8	258	2 G84858	floral homeodomain
4	806.5	63.9	248	2 T03592	floral homeotic pr
5	798.5	63.2	248	2 T07185	floral homeotic pr
6	794.5	62.9	242	2 JQ2212	pMADS3 protein - g
7	793	62.8	247	2 S60307	fbp6 protein - gar
8	781.5	61.9	239	2 A44343	promotes sex organ
9	752	59.5	284	2 T05033	floral homeotic pr
10	752	59.5	284	2 A85214	floral homeotic pr
11	751	59.5	252	2 A34844	probable transcrip
12	729.5	57.8	253	2 S57586	MADS-box regulator
13	729	57.7	262	2 T08039	MADS-box protein -
14	705	55.8	229	2 T08040	MADS-box protein 3
15	698.5	55.3	236	2 S59480	MADS-box protein C
16	695.5	55.1	254	2 T10185	MADS-box protein A
17	678	53.7	230	2 T04000	MADS-box protein d
18	670	53.0	259	2 T01700	floral homeotic pr
19	646.5	51.2	222	2 S51934	hypothetical prote
20	641	50.8	286	2 JQ2289	floral homeotic pr
21	627.5	49.7	265	2 T02261	MADS box protein -
22	582.5	46.1	258	2 PQ0770	floral homeotic pr
23	474	37.5	261	2 S1935	probable MADS-box
24	467	37.0	261	2 T09603	MADS-box protein 3
25	461.5	36.5	242	2 T09571	MADS box protein M
26	460	36.4	242	2 T10486	MADS box protein -
27	450.5	35.7	250	2 T04167	MADS box protein -
28	447.5	35.4	255	2 T03398	MADS box protein -
29	441	34.9	255	2 T03408	MADS box protein -

30 440.5 34.9 251 2 T00656 MADS box protein A
31 433 34.3 254 2 T10467 MADS box protein D
32 426 33.7 252 2 F39534 floral homeotic pr
33 426 33.7 273 2 T03410 MADS box protein -
34 424 33.6 224 2 J01690 MADS box protein f
35 421 33.3 224 2 S23728 MADS box protein t
36 418 33.1 250 2 T07100 MADS box protein h
37 416 32.9 242 2 S71757 MADS box protein D
38 415.5 32.9 245 2 T09569 MADS box protein M
39 415.5 32.9 249 2 T04307 M79 protein - rice
40 415.5 32.9 249 2 T04335 MADS box protein -
41 415 32.9 213 2 T10422 MADS box protein A
42 414.5 32.8 243 2 S71756 MADS box protein m
43 412.5 32.7 219 2 S46526 MADS box protein d
44 412 32.6 203 2 S51936 MADS-box protein d
45 412 32.6 257 2 S53306 MADS box protein M

RESULT 1
A39534
floral homeotic protein AGL1 [similarity] - Arabidopsis thaliana
N:Alternate names: agamous-like 1 AGL1; shatterproof 1 SHP1; T20N10.130
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jun-2000
C:Accession: A39534; T49161
R:Ma, H.; Yanofsky, M.F.; Meyerowitz, E.M.
Genes Dev. 5, 484-495, 1991
A:Title: AGL1-AGL6, an Arabidopsis gene family with similarity to floral homeotic and
A:Reference number: A39534; MUID:91160981; PMID:1672119
A:Accession: A39534
A:Molecule type: DNA
A:Residues: 1-248 <MAA>
A:Cross-references: GB:M55550; NID:g166587; PIDN:AAA32730.1; PID:g166588
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25017
A:Accession: T49161
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <DAN>
A:Cross-references: EMBL:AL353032; GSPDB:GN00061; ATSP:T20N10.130
A:Experimental source: cultivar Columbia; BAC clone T20N10
C:Genetics:
A:Gene: ATSP:T20N10.130
A:Map position: 3
A:Introns: 76/2; 103/3; 124/2; 157/3; 171/3; 185/3
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C:Keywords: DNA binding; nucleus; transcription regulation
F:17-72/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match	100.0%;	Score	1263;	DB 2;	Length	248;	
Best Local Similarity	100.0%;	Pred. No.	3.4e-81;				
Matches	248;	Conservative	0;	Mismatches	0;	Gaps	0;
QY	1	MEEGSSHDASSKKLGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVAL	60				
Db	1	MEEGSSHDASSKKLGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVAL	60				
QY	61	VIFSTRGLIYEYANNVSRGTIERYKKACSDAVNPSPVTEANTQYYQOEASKLRROIRDIQ	120				
Db	61	VIFSTRGLIYEYANNVSRGTIERYKKACSDAVNPSPVTEANTQYYQOEASKLRROIRDIQ	120				
QY	121	NSNRHIVGESLGSINFKELKNLEGRLEKGISRVRSKKNELLVAAIEYMKREMLQHNMM	180				
Db	121	NSNRHIVGESLGSINFKELKNLEGRLEKGISRVRSKKNELLVAAIEYMKREMLQHNMM	180				
QY	181	YLRAKIAEGARLNPDDQESSVIOQTGTTVYESGVSHDQSOQHYNRNYIPVNLLPEPNOQFSQ	240				
Db	181	YLRAKIAEGARLNPDDQESSVIOQTGTTVYESGVSHDQSOQHYNRNYIPVNLLPEPNOQFSQ	240				

QY 67 GRUYEVANNSVRGTIERYKKACSDAVNPPSPTEANTQYYQOEASKLRQIRDQNSNRHI 120
DB 68 GRUYEVANNSVKATIERYKKACSDSSNTGSTAEANAQYYQOEASKLRQIGLQNGNRNF 127

QY 127 VESLSGLNFKELKNLEGRLEKGISRVRSKKNELLVAEIEYMKREMELOHNNMYLRAKI 186
DB 128 LGESLAALNRLDLRNLEOKIEKGISKTRAKKNELLFAIEYMKREIDLHNNQNYLRAKI 187

QY 187 AGEARLNPDQOESSVIGTGTYYESGVSSH-----QSOHYNRNRYIPVNLEPNQOFSGDQ 242
DB 188 AETER-----SQOMNLMPGS-----SSDYLVPVQQSFDAARNYLQVGLQNTNNHYPRDQ 236

QY 243 PPLQLV 248
DB 237 PPLQLV 242

RESULT 7
S60307
fbp6 protein - garden petunia
C:Species: Petunia x hybrida (garden petunia)
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 24-Sep-1999
C:Accession: S60307
R:Angenent, G.C.; Franken, J.; Busscher, M.; Colombo, L.; van Tunen, A.J.
Plant J. 4, 101-112, 1993
A:Title: Petal and stamen formation in petunia is regulated by the homeotic
A:Reference number: S60307; MUID:94035167; PMID:8106081
A:Accession: S60307
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-247 <ANG>
A:Cross-references: EMBL:X68675; NID:g396198; PIDN:CA448635.1; PTD:g396199
C:Superfamily: transcription factor squa; serum response factor DNA-binding
F:18-73/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 62.8%; Score 793; DB 2; Length 247;
Best Local Similarity 68.6%; Pred. No. 2, 2e-48;
Matches 164; Conservative 27; Mismatches 46; Indels 2; Gaps

QY 10 AESSKKLGRGKTEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRL 69
DB 11 SSSQRKSGRGKTEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSSRGL 70

QY 70 YEVANNSVRGTIERYKKACSDAVNPPSPTEANTQYYQOEASKLRQIRDQNSNRHIVE 129
DB 71 YEVANNSVRATIDRYKKHADSTSGVSEANTQYYQOEAAKLRRQIRDIOTYNRQIIVE 130

QY 130 SLGSLNFKELKNLEGRLEKGISRVRSKKNELLVAEIEYMKREMELOHNNMYLRAKIAEG 189
DB 131 ALSLSLSPRLKNLEGLKAIGRVRSKKNELVSEIELMKREIEMQANMYLRAKIAEV 190

QY 190 ARLNPDQOESSVIGTGTYYESGVSSHQSOHYNRNRYIPVNLEPNQOFSGDQPLQLV 248
DB 191 ERAT--QQMNLMHGGGSEYQQQPMSSTSQPYDARNFLPVLNLEPNPHYSRQDQTALQLV 247

RESULT 8
A44343
promotes sex organ development protein ple - garden snapdragon
C:Species: Antirrhinum majus (garden snapdragon)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 16-Jul-1999
C:Accession: A44343
R:Bradley, D.; Carpenter, R.; Sommer, H.; Hartley, N.; Coen, E.
Cell 72, 85-95, 1993
A:Title: Complementary floral homeotic phenotypes result from opposite ori
A:Reference number: A44343; MUID:93137332; PMID:8093684
A:Accession: A44343
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-239 <BRA>
A:Cross-references: GB:S53900; NID:g264222; PIDN:AAB25101.1; PID:g264223
A>Note: sequence extracted from NCBI backbone (NCBIP:123356)

A;Residues: 1-252 <MAN>
A;Cross-references: GB:M99415; NID:q167125; PIDN:AAA32985.1; PID:g167126
A;Note: sequence extracted from NCBI backbone (NCBIP:115468)
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C;Keywords: DNA binding; nucleus; transcription regulation
F:18-73/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 59.5%; Score 751; DB 2; Length 252;
Best Local Similarity 62.0%; Pred. No. 1.9e-45;
Matches 158; Conservative 34; Mismatches 49; Indels 14; Gaps 5;

Qy 1 MEEGSSHDAESSKILGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVAL 60
Db 5 MELGGES---SPQRAGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVAL 61

Qy 61 VIFSTRGLYEVANNSVCTIERYKKACSDAVNPPSVTEANTQYQOEASKLRQIRDIQ 120
Db 62 IVFSRGLRYEYNSNVKCTIERYKKAISDNSTGVSVAETNAQYQOESAKLRQIIISIQ 121

Qy 121 NSNRHIVGESLGNFKELKNLEGRLEKISRVRSKKNELLVAEIEYMKREMELOHNNM 180
Db 122 NSNRQLMGETIGSMSPKELNLEGRLDNRVNRIRSKKNELLFAEIDYMKREVDLHNDQ 181

Qy 181 YLRAKIAGARLNPDQESSVIGTGTTVYSGVSSHQSOHY---NRRNYIPVNLLEPNQOF 237
Db 182 LLRAKIAENERNPSM---SLMPGGSNYEO--IMPPQTQPPFDSRNYFOVAALQPNHH 237

Qy 238 ---SGQPPLQLV 248
Db 238 YSSAGREDOTALQLV 252

RESULT 12
S57586
MADS-box regulatory protein - Rumex acetosa
C;Species: Rumex acetosa
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Sep-1999
C;Accession: S57586
R;Ainsworth, C.; Thangavelu, M.; Crossley, S.; Buchanan-Wollaston, V.; Parker, J.
submitted to the EMBL Data Library, June 1995
A;Description: Male and female flowers from the dioecious plant Rumex acetosa show diffe
A;Reference number: S57586
A;Accession: S57586
A;Molecule type: mRNA
A;Residues: 1-253 <AIN>
A;Cross-references: EMBL:X89107; NID:g887578; PIDN:CAA61480.1; PID:g887579
C;Genetics:
A;Gene: P1
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C;Keywords: DNA binding; nucleus; transcription regulation
F:21-76/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 57.8%; Score 729.5; DB 2; Length 253;
Best Local Similarity 61.5%; Pred. No. 6.1e-44;
Matches 152; Conservative 37; Mismatches 45; Indels 13; Gaps 4;

Qy 9 DAESSKILGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVFSTRGR 68
Db 13 DGSPQRMGKRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVFSRGR 72

Qy 69 LYEVANNSVCTIERYKKACSDAVNPPSVTEANTQYQOEASKLRQIRDIQ----NSNR 124
Db 73 LYEVANNSVKTATIERKKYKTCSDSTGVTGVSVEANA---QOEAAKLRNQIRLTQNTNTR 129

Qy 125 HIVGESLGNFKELKNLEGRLEKISRVRSKKNELLVAEIEYMKREMELOHNNMYLRA 184
Db 130 NLMGEGTSMNKKDLNLETRLEKIGISRVRKKNELLFAEIEYMKREMELOHNNMYLRA 189

Qy 185 KIAEGARLNPDQESSVIGTGTTVYSGVSSHQSOQ---HYNRRNYIPVNLLEPNQOFSQD 241
Db 190 KIAESER---SQSNMLMPGSSGQHVELMFPQSQAGPDSRNFQVSDLPDPERYSCQN 246

Qy 242 QPPLQLV 248

Db 247 QTPLQLV 253

RESULT 13
T08039
MADS-box protein - cucumber
C;Species: Cucumis sativus (cucumber)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C;Accession: T08039
R;Kater, M.M.; Colombo, L.; Franken, J.; Busscher, M.; Masiero, S.; van Lookeren Camp
Plant Cell 10, 171-182, 1998
A;Title: Multiple AGAMOUS homologs from cucumber and petunia differ in their ability
A;Reference number: Z16308; MUID:98158685; PMID:9490741
A;Accession: T08040
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-262 <KAT>
A;Cross-references: EMBL:AF035438; NID:g2997612; PIDN:AAC08528.1; PID:g2997613
C;Genetics:
A;Gene: CUM1
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C;Keywords: DNA binding; nucleus; transcription regulation
F:43-98/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 57.7%; Score 729; DB 2; Length 262;
Best Local Similarity 64.6%; Pred. No. 7e-44;
Matches 153; Conservative 31; Mismatches 37; Indels 16; Gaps 3;

Qy 14 KILGRKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVFSTRGRLYEYA 73
Db 40 RKMGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVFSRGRLYEYA 99

Qy 74 NNSVRGTIERYKKACSDAVNPPSVTEANTQYQOEASKLRQIRDIQNSNRHIVGESLGS 133
Db 100 NNSVKATIDRYKKASDSSNTGSTSEANTQYQOEAAKLRVQIGNLQNSNRNMLGESLSS 159

Qy 134 LNFKEKLNLEGRLEKISRVRSKKNELLVAEIEYMKREMELOHNNMYLRAKIAEGAR-L 192
Db 160 LTKADKLGLETKLEKIGISRIRSKKNELLFAEIEYMKRREIDLHNNNNMLRAKIAESERNV 219

Qy 193 NPDQESSVIGTGTTVYSGVSSHQSOHYN-RNTPVNLLEPNQOFSQDQPPQLQV 248
Db 220 NMMGGFEFLM-----QSHPYDPRDFQVNGLNQHNHOYPRDNNALQLV 262

RESULT 14
T08040
MADS-box protein - cucumber
C;Species: Cucumis sativus (cucumber)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C;Accession: T08040
R;Kater, M.M.; Colombo, L.; Franken, J.; Busscher, M.; Masiero, S.; van Lookeren Camp
Plant Cell 10, 171-182, 1998
A;Title: Multiple AGAMOUS homologs from cucumber and petunia differ in their ability
A;Reference number: Z16308; MUID:98158685; PMID:9490741
A;Accession: T08040
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-229 <KAT>
A;Cross-references: EMBL:AF035439; NID:g2997614; PIDN:AAC08529.1; PID:g2997615
C;Genetics:
A;Gene: CUM10
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C;Keywords: DNA binding
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 55.8%; Score 705; DB 2; Length 229;
Best Local Similarity 60.1%; Pred. No. 2.8e-42;
Matches 143; Conservative 44; Mismatches 35; Indels 16; Gaps 4;

Qy 16 LGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVFSTRGRLYEYANN 75
:|||||

```
Db 1 MGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSRGRLEYEYNN 60
QY 76 SVRGTIERYKKACSDAVNPSPVTEANTQYQOEASKLRQIRDIQNSN----RHIVGESL 131
Db 61 SIKTTIERYKKACSDSSATSTELNTQYQOESAKLRQIQMLQNSNSNLVRHLMGDSL 120
QY 132 GSLNFKELKNLEGRLEKISRVRKKNELLVAEIEYMKREMELOHNNMYLRAKIAEGAR 191
Db 121 SALTVELKQLLENLERGIRIRSKKHMEMLAEIEYLOKREIELENNVCIRTKAEVER 180
QY 192 LNPDQOESSVTQGTTVYESGVSHDQSHYRNRYIPVNLLEP--NQQFSGGQDPLQL 247
Db 181 V----QOANMVSQGL-----NAIQALANSRNFSPNIMEPAGPVSYSHQDKKMLHL 228

RESULT 15
S59480
MADS-box protein 3 - rice
C:Species: Oryza sativa (rice)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 28-May-1999
C:Accession: S59480
R:Kang, H.G.; Noh, Y.S.; Chung, Y.Y.; Costa, M.A.; An, K.; An, G.
Plant Mol. Biol. 29, 1-10, 1995
A:Title: Phenotypic alterations of petal and sepal by ectopic expression of a rice MADS
A:Reference number: S59480; MUID:96017609; PMID:7579155
A:Accession: S59480
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-236 <KAN>
A:Cross-references: GB:L37528; NID:g886404; PIDN:AAA99964.1; PID:g886405
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
F:2-57/Domain: serum response factor DNA-binding domain homology <SRE>

Query Match 55.38; Score 698.5; DB 2; Length 236;
Best Local Similarity 59.74; Pred. No. 8.2e-42;
Matches 141; Conservative 47; Mismatches 37; Indels 11; Gaps 5;

QY 16 LGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSTRGRLEYEYANN 75
Db 1 MGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSRGRLEYEYANN 60
QY 76 SVRGTIERYKKACSDAVNPSPVTEANTQYQOEASKLRQIRDIQNSN-RHIVGESLGL 134
Db 61 SVKSTVERYKKANSDTNSGTVAEYNAQHYQOESSKLRQIQISLQNSNSTIVGDSINTM 120
QY 135 NFKELKNLEGRLEKISRVRKKNELLVAEIEYMKREMELOHNNMYLRAKIAEGARLNP 194
Db 121 SLRDLKQVENLEKGIARIRKKNELLVAEIEYMKREVELQNDNDNNMYLRSKVENER--- 177
QY 195 DQOESSVI--QGTTVYESGVSHDQSHYRNRYIPVNLLEPNQOFGQDQP-PLQL 247
Db 178 GQQLPLNMGAASTSEYDHVN---NPYDSRNFQVNIQQPHVAHQLPQTTLQL 229

Search completed: January 27, 2003, 12:46:15
Job time : 14.5587 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 27., 2003, 12:39:28 ; Search time 31.6275 Seconds
(without alignments)
1044.854 Million cell updates/sec

Title: US-09-978-382A-4
Perfect score: 1263
Sequence: 1 MEEGSSHDAESSKILGRK.....NLLEPNQFSGQDPPIQLIV 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

1:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
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13:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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21:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1263	100.0	248	20 AAW80999	Arabidopsis AGL1 p
2	1263	100.0	248	21 AAG09411	Arabidopsis thalia
3	1050	83.1	246	20 AAW81000	Arabidopsis AGL5 p
4	1046	82.8	258	21 AAG32583	Arabidopsis thalia
5	830.5	65.8	251	17 AAR99633	Eucalyptus AGE-1 p
6	769.5	60.9	241	21 AAY58656	Poplar PTAG-1 flor
7	769.5	60.9	241	22 AAB68437	Amino acid sequenc
8	769.5	60.9	241	23 ABG30867	Poplar floral home
9	752	59.5	300	21 AAG52721	Arabidopsis thalia
10	739.5	58.6	238	21 AAY58657	Poplar PTAG-2 flor

11	739.5	58.6	238	22 AAB68438	Amino acid sequenc
12	739.5	58.6	238	23 ABG30868	Poplar floral home
13	722	57.2	221	21 AAY44804	Petunia hybrida ne
14	722	57.2	221	21 AAY58648	Petunia nectary-sp
15	712.5	56.4	264	23 ABG60988	Novel floral meris
16	695.5	55.1	257	21 AAG33135	Zea mays protein f
17	695.5	55.1	260	21 AAG33134	Zea mays protein f
18	695.5	55.1	283	21 AAG33133	Zea mays protein f
19	689.5	54.6	268	23 ABG60931	Novel floral meris
20	680	53.8	277	21 AAG16689	Arabidopsis thalia
21	680	53.8	277	21 AAG40212	Arabidopsis thalia
22	679.5	53.8	185	21 AAB32638	Eucalyptus grandis
23	678	53.7	230	21 AAG16690	Arabidopsis thalia
24	678	53.7	230	21 AAG40213	Arabidopsis thalia
25	663.5	52.5	229	17 AAR99637	Eucalyptus AGE-2 p
26	651.5	51.6	222	21 AAB26795	Plant reproductive
27	628	49.7	133	21 AAG07156	Arabidopsis thalia
28	626.5	49.6	268	21 AAG43856	Zea mays protein f
29	555	43.9	161	21 AAB33229	Eucalyptus grandis
30	503	39.8	142	21 AAG12611	Zea mays protein f
31	503	39.8	155	21 AAG12609	Zea mays protein f
32	486	38.5	122	21 AAG37576	Arabidopsis thalia
33	473.5	37.5	260	23 ABG60946	Novel floral meris
34	467	37.0	261	19 AAW48623	Pinus radiata cone
35	461.5	36.5	242	19 AAW48622	Pinus radiata cone
36	458	36.3	205	23 ABG60922	Novel floral meris
37	453	35.9	260	21 AAG17603	Arabidopsis thalia
38	452.5	35.8	181	21 AAB33310	Pinus radiata tran
39	451.5	35.7	260	21 AAG40277	Arabidopsis thalia
40	450.5	35.7	250	21 AA017679	Plant flowering ti
41	447	35.4	269	21 AAY84911	Amino acid sequenc
42	445	35.2	281	21 AAG29741	Arabidopsis thalia
43	442	35.0	250	21 AAG17604	Arabidopsis thalia
44	440.5	34.9	251	21 AAG40278	Arabidopsis thalia
45	431	34.1	241	17 AAR96962	NEMADS3 protein.

ALIGNMENTS

RESULT 1
AAW80999
ID AAW80999 standard; Protein; 248 AA.

AC AAW80999;

DT 10-MAY-1999 (first entry)

DE Arabidopsis AGL1 polypeptide.

XX AGL1-like gene; agamous-like 1 gene; seed dispersal; dehiscence; transgenic plant.

OS Arabidopsis thaliana.

PN WO9900502-A1.

PD 07-JAN-1999.

XX 25-JUN-1998; 98WO-US13208.

PR 28-APR-1998; 98US-0067800.

XX 27-JUN-1997; 97US-0051030.

(REGC) UNIV CALIFORNIA.

Ferrandiz C, Yanofsky MF;

WPI; 1999-095747/08.

DR N-PSDB; AAV99857, AAV99859.

Use of agamous-like nucleic acids - useful for the production of transgenic seed plants in which dehiscence is modified resulting in

```
PT delayed seed dispersal
XX
PS Disclosure; Page 88-89; 126pp; English.
XX
CC This is the deduced amino acid sequence of an Arabidopsis
CC agamous-like 1 (AGL1) polypeptide that is involved in the
CC regulation of dehiscence. A cDNA clone encoding AGL1 is provided
CC in AAV99859, and a genomic clone in AAV99857. The invention provides a
CC transgenic seed plant, such as an agl1 and agl5 double mutant, that
CC is characterised by delayed seed dispersal due to suppression of
CC AGL1 and AGL5 (see AAM01000) expression. The invention also provides
CC dehiscence zone regulatory elements, derived from the AGL1 or AGL5
CC gene, that confer selective expression upon an operatively linked
CC nucleic acid molecule in the valve margin or dehiscence zone of a
CC seed plant. The transgenic seed plants include members of the
CC Brassicaceae, such as rapeseed, and members of the Fabaceae, such
CC as soybean, pea, lentil and bean. A plant expression vector
CC comprising a dehiscence zone-selective regulatory element, and a
CC kit for producing the transgenic seed plants are also provided.
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 1263; DB 20; Length 248;
Best Local Similarity 100.0%; Pred. No. 5.6e-116;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEEGSSHDAESSKLGKTEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVAL 60
   |||||

QY 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPSVTEANTQYYQOEASKLRRQRIDIQ 120
   |||||
DB 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPSVTEANTQYYQOEASKLRRQRIDIQ 120
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QY 121 NSNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKNELLVAEIYMQKREMELOHNNM 180
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QY 181 YLRAKIAGARLNPDQOESSVIOGTTVYESGVSSHDSQSOHYNRNYPVNLLEPNQOFSGQ 240
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DB 181 YLRAKIAGARLNPDQOESSVIOGTTVYESGVSSHDSQSOHYNRNYPVNLLEPNQOFSGQ 240
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QY 241 DOPPLQLV 248
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DB 241 DOPPLQLV 248
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RESULT 2
AAG09411
ID AAG09411 standard; Protein: 248 AA.
AC AAG09411;
XX
XX 17-OCT-2000 (first entry)
DT
DE
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7335.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
PD
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
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PR 23-MAR-1999; 99US-0125788.
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Query Match 100.0%; Score 1263; DB 21; Length 248;
Best Local Similarity 100.0%; Pred. No. 5.6e-116;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEEGGSSHDAESSKLGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVAL 60

Qy 61 VIFSTRGRLYEYANNVRGTIERYKKACSDAVNPPSVTEANTQYQQEASKLRQIRDQ 120
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Db 121 NSNRHIVGESLGNFKELKNLEGRLEKISRVRKSKNELLVAEIYMKREMELOHNNM 180

Qy 181 YLRAKIAEGARLNPDOQESSVIQCTTVYESGVSHDSQHYNNRNPVNNLEPNQOQFSGQ 240
Db 181 YLRAKIAEGARLNPDOQESSVIQCTTVYESGVSHDSQHYNNRNPVNNLEPNQOQFSGQ 240

Qy 241 DQPLQLV 248
Db 241 DQPLQLV 248

RESULT 3
AAW81000
ID AAW81000 standard; Protein; 246 AA.
XX AC AAW81000;
XX DT 10-MAY-1999 (first entry)
XX DE Arabidopsis AGL5 polypeptide.
XX DE AGL5-like gene; agamous-like 5 gene; seed dispersal; dehiscence;
XX KW transgenic plant.
XX OS Arabidopsis thaliana.
XX PN W09900502-A1.
XX

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PD 07-JAN-1999.
XX
PF 25-JUN-1998; 98W0-US13208.
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PR 28-APR-1998; 98US-0067800.
PR 27-JUN-1997; 97US-0051030.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Ferrandiz C, Yanofsky MF;
XX WPI: 1999-095747/08.
DR N-PSDB; AAV99858, AAV99860.
XX
PT Use of agamous-like nucleic acids - useful for the production of
PT transgenic seed plants in which dehiscence is modified resulting in
PT delayed seed dispersal
XX
PS Disclosure; Page 91-92; 126pp; English.
XX
CC This is the deduced amino acid sequence of an Arabidopsis
CC agamous-like 5 (AGL5) polypeptide that is involved in the
CC regulation of dehiscence. A cDNA clone encoding AGL5 is provided
CC in AAV99860, and a genomic clone in AAV99858. The invention provides a
CC transgenic seed plant, such as an agl1 and agl5 double mutant, that
CC is characterised by delayed seed dispersal due to suppression of
CC AGL1 (see AAV80999) and AGL5 expression. The invention also provides
CC dehiscence zone regulatory elements, derived from the AGL1 or AGL5
CC gene, that confer selective expression upon an operatively linked
CC nucleic acid molecule in the valve margin or dehiscence zone of a
CC seed plant. The transgenic seed plants include members of the
CC Brassicaceae, such as rapeseed, and members of the Fabaceae, such
CC as soybean, pea, lentil and bean. A plant expression vector
CC comprising a dehiscence zone-selective regulatory element, and a
CC kit for producing the transgenic seed plants are also provided.
XX
SQ Sequence 246 AA;

Query Match 83.1%; Score 1050; DB 20; Length 246;
Best Local Similarity 85.5%; Pred. No. 5.2e-95;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

Qy 1 MEEGSSHDAESKGLRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60
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Qy 121 NSNRHVGESLGSNFKELKNGLEKRGISRVRSKKNELLVAEIEYMKREMLQHNMM 180
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Qy 181 YLRAKIAGBARLNPDQSSVIQGTVTYVSGVSHDQSOHYNNRNPVNLLEPNQOFSQ 240
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Qy 241 DQPLQLV 248
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Db 239 DQPLQLV 246
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RESULT 4
AAG32583
ID AAG32583 standard; Protein; 258 AA.
XX
AC AAG32583;
XX
DT 17-Oct-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39337.
XX
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 24-JUN-1999;	99US-0140695.	PR 07-SEP-1999;	99US-0152363.
PR 28-JUN-1999;	99US-0140823.	PR 10-SEP-1999;	99US-0153070.
PR 29-JUN-1999;	99US-0140991.	PR 13-SEP-1999;	99US-0153758.
PR 30-JUN-1999;	99US-0141287.	PR 15-SEP-1999;	99US-0154018.
PR 01-JUL-1999;	99US-0141842.	PR 16-SEP-1999;	99US-0154039.
PR 01-JUL-1999;	99US-0142154.	PR 20-SEP-1999;	99US-0154779.
PR 02-JUL-1999;	99US-0142055.	PR 22-SEP-1999;	99US-0155139.
PR 06-JUL-1999;	99US-0142390.	PR 23-SEP-1999;	99US-0155486.
PR 08-JUL-1999;	99US-0142803.	PR 24-SEP-1999;	99US-0155659.
PR 09-JUL-1999;	99US-0142920.	PR 28-SEP-1999;	99US-0156458.
PR 12-JUL-1999;	99US-0142977.	PR 29-SEP-1999;	99US-0156596.
PR 13-JUL-1999;	99US-0143542.	PR 04-OCT-1999;	99US-0157117.
PR 14-JUL-1999;	99US-0143624.	PR 05-OCT-1999;	99US-0157753.
PR 15-JUL-1999;	99US-0144005.	PR 06-OCT-1999;	99US-0157865.
PR 16-JUL-1999;	99US-0144085.	PR 07-OCT-1999;	99US-0158029.
PR 16-JUL-1999;	99US-0144086.	PR 08-OCT-1999;	99US-0158232.
PR 19-JUL-1999;	99US-0144325.	PR 12-OCT-1999;	99US-0158369.
PR 19-JUL-1999;	99US-0144331.	PR 13-OCT-1999;	99US-0159293.
PR 19-JUL-1999;	99US-0144332.	PR 13-OCT-1999;	99US-0159294.
PR 19-JUL-1999;	99US-0144333.	PR 13-OCT-1999;	99US-0159295.
PR 19-JUL-1999;	99US-0144334.	PR 14-OCT-1999;	99US-0159329.
PR 19-JUL-1999;	99US-0144335.	PR 14-OCT-1999;	99US-0159330.
PR 20-JUL-1999;	99US-0144352.	PR 14-OCT-1999;	99US-0159331.
PR 20-JUL-1999;	99US-0144632.	PR 14-OCT-1999;	99US-0159637.
PR 20-JUL-1999;	99US-0144814.	PR 18-OCT-1999;	99US-0159638.
PR 21-JUL-1999;	99US-0145086.	PR 21-OCT-1999;	99US-0159584.
PR 21-JUL-1999;	99US-0145088.	PR 21-OCT-1999;	99US-0160741.
PR 22-JUL-1999;	99US-0145085.	PR 21-OCT-1999;	99US-0160767.
PR 22-JUL-1999;	99US-0145089.	PR 21-OCT-1999;	99US-0160768.
PR 22-JUL-1999;	99US-0145192.	PR 21-OCT-1999;	99US-0160770.
PR 23-JUL-1999;	99US-0145145.	PR 21-OCT-1999;	99US-0160814.
PR 23-JUL-1999;	99US-0145218.	PR 21-OCT-1999;	99US-0160815.
PR 23-JUL-1999;	99US-0145224.	PR 22-OCT-1999;	99US-0160980.
PR 26-JUL-1999;	99US-0145276.	PR 22-OCT-1999;	99US-0160981.
PR 27-JUL-1999;	99US-0145913.	PR 25-OCT-1999;	99US-0160989.
PR 27-JUL-1999;	99US-0145918.	PR 25-OCT-1999;	99US-0161404.
PR 27-JUL-1999;	99US-0145919.	PR 25-OCT-1999;	99US-0161405.
PR 28-JUL-1999;	99US-0145951.	PR 25-OCT-1999;	99US-0161406.
PR 02-AUG-1999;	99US-0146386.	PR 26-OCT-1999;	99US-0161359.
PR 02-AUG-1999;	99US-0146388.	PR 26-OCT-1999;	99US-0161360.
PR 02-AUG-1999;	99US-0146389.	PR 26-OCT-1999;	99US-0161361.
PR 03-AUG-1999;	99US-0147038.	PR 28-OCT-1999;	99US-0161920.
PR 04-AUG-1999;	99US-0147204.	PR 28-OCT-1999;	99US-0161992.
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PR 05-AUG-1999;	99US-0147260.		
PR 06-AUG-1999;	99US-0147303.		
PR 06-AUG-1999;	99US-0147416.		
PR 09-AUG-1999;	99US-0147493.		
PR 09-AUG-1999;	99US-0147935.		
PR 10-AUG-1999;	99US-0148171.		
PR 11-AUG-1999;	99US-0148319.		
PR 12-AUG-1999;	99US-0148341.		
PR 13-AUG-1999;	99US-0148565.		
PR 13-AUG-1999;	99US-0148684.		
PR 16-AUG-1999;	99US-0149368.		
PR 17-AUG-1999;	99US-0149175.		
PR 18-AUG-1999;	99US-0149426.		
PR 20-AUG-1999;	99US-0149722.		
PR 20-AUG-1999;	99US-0149723.		
PR 20-AUG-1999;	99US-0149929.		
PR 23-AUG-1999;	99US-0149902.		
PR 23-AUG-1999;	99US-0149930.		
PR 23-AUG-1999;	99US-0150566.		
PR 26-AUG-1999;	99US-0150884.		
PR 27-AUG-1999;	99US-0151065.		
PR 27-AUG-1999;	99US-0151066.		
PR 30-AUG-1999;	99US-0151080.		
PR 31-AUG-1999;	99US-0151303.		
PR 31-AUG-1999;	99US-0151438.		

Query Match

Best Local Similarity

Matches 21l; Conservative

82.8%;

Score 1046;

DB 21;

Length 258;

Pred. No. 1.4e-94;

Mismatches 12;

Indels 2;

Gaps 1;

Qy 1	MEEGSSHDAESSKLGKRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVCDAEVAL	60
Db 1	MEGGASNEVAESSKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVCDAEVAL	60
Qy 61	VIFSTGRLYEYANNVSRGTIERYKKACSDAVNPPSVTEANTQYQOASKLRRQIRDIQ	120
Db 61	VIFSTGRLYEYANNVSRGTIERYKKACSDAVNPPTEANTQYQOASKLRRQIRDIQ	120
Qy 121	NSNRHIVGESLGNFKELNLEGRLEKISRVRSKKNELVAETEMQKREMELOHNNM	180
Db 121	NLNRHILGESLGNFKELNLESRLEKISRVRSKKHEMLVAETEMQKREIELONDNM	180
Qy 181	YLRAKIAEGARLNPDQOESSVIQGTIVYESGVSHDQSOHYNRNYPVYNLLEPNQOFSQ	240
Db 181	YLRSKITE--RTGLQOQESSVIHQGTIVYESGVTSHQSGQYNNRYIAVNLLEPNQNSNQ	238
Qy 241	DQPPLQL 247	
Db 239	DQPPLQL 245	


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PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 27-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147036.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.

PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 59.5%; Score 752; DB 21; Length 300;
Best Local Similarity 63.2%; Pred. No. 1.6e-65;
Matches 160; Conservative 33; Mismatches 48; Indels 12; Gaps 5;

Qy 2 EGGSSHDAESSKGLRGKTEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALV 61
Db 54 ELGG---DSSPLKSGRGKTEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALI 110
Qy 62 IFSTRGLYEYANNSVGTIERYKKACSDAVNPSPVTEANTQYYQOEASKLRRQIRDION 121
Db 111 VFSSRGLYEYSNNSVKGTIERYKKALSDNSNTSGVAEINQAQYYQESAKLRQIISION 170
Qy 122 SNRHVGESIGSLNFELKNLEGRLEKGISRVRSKKNELLVAEIYQKREMELOHNNMY 181
Db 171 SNRQLMGETIGSMPEKLRNLEGRLEKISITRIRSKKNELLFSEIDYQKREYDLHDNDQI 230
Qy 182 LRAKIAEGARLNPDQOESSVIOGTTVYESGV-SSHDQSOHY-NRNYIPVNLLPNOQF-- 237
Db 231 LRAKIAENERNP---SISLMPGSGSYEQMLPPPTQSQPDSRNYFOVALQPNHHYS 287
Qy 238 ---SGQDQPPQLV 248
Db 288 SAGRQDQTALQLV 300

RESULT 10
AAV58657
ID AAV58657 standard; Protein; 238 AA.
XX
AC AAV58657;
XX
DT 11-APR-2000 (first entry)
XX
DE Poplar PTAG-2 floral homeotic gene-encoded protein.
XX
KW Poplar; PTAG-2; floral homeotic gene; transgenic plant; sterility;
XX
OS Populus balsamifera subsp. trichocarpa.
XX
FH key Location/Qualifiers
```

FT Domain 17..33
FT /note= "MADS domain"
FT Domain 106..172
FT /note= "K domain"
PN CA2227940-A1.
XX
XX
PD 06-OCT-1999.
XX
XX 07-APR-1998; 98CA-2227940.
PF
XX 06-APR-1998; 98US-0080851.
PR
XX (UYOR-) UNIV OREGON HEALTH SCI.
PA
XX Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;
PI WPI; 2000-106662/10.
XX N-PSDB; AAZ57848, AAZ57949.
DR
XX Nucleic acid from Populus trichocarpa genes, useful for producing
XX transgenic plants, particularly trees, with modified fertility
XX characteristics such as sterility -
PT
XX
XX Claim 31; Page 77; 92pp; English.
XX
XX The present sequence is that of the novel PTAG-2 protein of poplar
XX (Populus balsamifera subsp. trichocarpa), as deduced from newly
XX isolated gene and cDNA sequences (see AAZ57948-49). PTAG-2 is 1
XX of 4 novel floral homeotic genes identified in this poplar species.
XX It is a homologue of AGAMOUS and is expressed in floral tissues.
XX PTAG-2 contains a MADS domain and a K-domain. The invention
XX provides nucleic acid sequences of the 4 novel Populus genes, the
XX corresponding cDNA sequences (see AAZ47942-49) and deduced amino acid
XX sequences (see AAY58434-37). It also provides methods of using the
XX gene and cDNA sequences to produce genetically engineered Populus
XX and other trees having modified fertility characteristics, including
XX sterility. Genetic constructs useful in producing genetically
XX engineered Populus and other trees include antisense versions of
XX PTAG-2, dominant negative mutants, and constructs useful for sense
XX suppression. Sterile trees allow increased wood yield and a
XX reduction in the production of allergens such as pollen.
XX
XX Sequence 238 AA;
SQ
Query Match 58.6%; Score 739.5; DB 21; Length 238;
Best Local Similarity 65.5%; Pred. No. 1.9e-64;
Matches 154; Conservative 34; Mismatches 36; Indels 11; Gaps 4;
Qy 11 ESS--KKLGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGR 68
Db 9 ESSPLRLKGRGKVEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGR 68
Qy 69 LYEYANNSVRGTIERYKKACSDAVNPPSVTEANTQYQOEASKLRQIRDIONSNRHIVG 128
Db 69 LYEYSNNVSKSTIERYKKACADSSNNGSVSEANAQFYQOEAAKLRSQIGNLQNSNRMLG 128
Qy 129 ESLGSLNFKELNLEGRLEKIGISRSVRKKNELLVAEIEYMQKREMELOHNNMYLRAKIAE 188
Db 129 ELSLSLVKELKSLKLEIKLEKIGIRISKKNELLFAEIEYMQKREIDLHNNQLLRKIAE 188
Qy 189 GARLNPQOESSVIQGTIVYESGVSSHQSOHY -NRNYIPVNLLEPNQOFSQDQ 242
Db 189 NER---KRQHNLMPGGVNFET----MQSQPFDSRNSQVNGLPANHYPHEDQ 235
RESULT 11
AAB68438
ID AAB68438 standard; Protein; 238 AA.
XX
XX AAB68438;
XX
XX 23-JUL-2001 (first entry)
DT

XX Amino acid sequence of the floral homeotic protein PTAG-2.
DE
XX
XX Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;
KW LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
KW fertility; sterility.
XX
XX Populus balsamifera.
XX
XX Key Location/Qualifiers
FH Domain 16..72
FT /note= "MADS domain"
FT Domain 106..172
FT /note= "K-domain"
XX
XX CA2319853-A1.
PN
XX
XX 01-APR-2001.
PD
XX
XX 02-OCT-2000; 2000CA-2319853.
PF
XX
XX 01-OCT-1999; 99US-0410464.
PR
XX (UYOR-) UNIV OREGON HEALTH SCI.
PA
XX
XX Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
PI WPI; 2001-336098/36.
XX N-PSDB; AAF85400, AAF85401, AAF85402.
DR
XX Novel isolated polynucleotide derived from Populus species, useful for
XX producing transgenic plants having modified fertility characteristic,
XX particularly sterility -
PT
XX
XX Claim 23; Page 62-63; 69pp; English.
PS
XX
XX The present sequence represents a floral homeotic protein, designated
XX PTAG-2, which is derived from Populus balsamifera subsp. trichocarpa.
XX The specification also describes PTD, PTLF, and PTAG-1 proteins. The
XX floral homeotic proteins are expressed in floral tissues. PTLF is a
XX homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in
XX immature inflorescences on which floral primordia are developing. PTD
XX is a homologue of DEFICIENS (DEF), and is strongly expressed in stamen
XX primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
XX homologues of AGAMOUS (AG). The floral homeotic proteins and
XX polynucleotides are useful for producing transgenic plants having
XX modified fertility characteristics, particularly sterility.
XX
XX Sequence 238 AA;
SQ
Query Match 58.6%; Score 739.5; DB 22; Length 238;
Best Local Similarity 65.5%; Pred. No. 1.9e-64;
Matches 154; Conservative 34; Mismatches 36; Indels 11; Gaps 4;
Qy 11 ESS--KKLGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGR 68
Db 9 ESSPLRLKGRGKVEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGR 68
Qy 69 LYEYANNSVRGTIERYKKACSDAVNPPSVTEANTQYQOEASKLRQIRDIONSNRHIVG 128
Db 69 LYEYSNNVSKSTIERYKKACADSSNNGSVSEANAQFYQOEAAKLRSQIGNLQNSNRMLG 128
Qy 129 ESLGSLNFKELNLEGRLEKIGISRSVRKKNELLVAEIEYMQKREMELOHNNMYLRAKIAE 188
Db 129 ELSLSLVKELKSLKLEIKLEKIGIRISKKNELLFAEIEYMQKREIDLHNNQLLRKIAE 188
Qy 189 GARLNPQOESSVIQGTIVYESGVSSHQSOHY -NRNYIPVNLLEPNQOFSQDQ 242
Db 189 NER---KRQHNLMPGGVNFET----MQSQPFDSRNSQVNGLPANHYPHEDQ 235
RESULT 12
ABG30868

CC and the desired protein is easily recovered from it. The recombinant
CC proteins are useful for pharmaceutical purposes, as enzymes for biotests
CC and antioxidants for food additives.

XX SQ Sequence 221 AA;
Query Match 57.2%; Score 722; DB 21; Length 221;
Best Local Similarity 64.7%; Pred. No. 9e-63;
Matches 152; Conservative 30; Mismatches 37; Indels 16; Gaps 3;
QY 16 LGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLEYANN 75
Db 1 MGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLEYANN 60
QY 76 SVRGTIERYKKACSDAVNPPSVTEANTOYQOEASKLRQIRDIONSNRHIVGESLSLN 135
Db 61 SVKATIDRYKKASSDSSNTGSTSEANTQYQOEAKLRVQIGNLQNSNRMLGESLSLT 120
QY 136 FKEKLNLEGRLEKISRVRSKKNELLVAEIEYMKRELOHNNMYLRAKIAEGAR-LNP 194
Db 121 AKDLKGLTKLEKIGISRIRSKKNELLFAEIEYMRKREIDLHNNQMLRAKIAESERNVM 180
QY 195 DQESSVIOGTTVYVESGVSHDQSOHYN-RNYIPVNLEPNQOFSQDQPPLOLV 248
Db 181 MGGEFELM-----QSHPYDPRDFQVNGLQHNHQYPRQDNMALQLV 221

RESULT 14
AAV58648
ID AAV58648 standard; Protein; 221 AA.
XX AC AAV58648;
XX DT 11-APR-2000 (first entry)
DE Petunia nectary-specific FBP15 protein.
XX FBP14; nectary; nectar; transgenic plant; honey.
XX Petunia hybrida.
XX EP974667-A1.
XX 26-JAN-2000.
XX 16-JUL-1998; 98EP-0202375.
XX 16-JUL-1998; 98EP-0202375.
XX (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.
XX Creemers J, Angenent GC, Kater MM;
XX WPI; 2000-108400/10.
XX N-PSDB; AAZ35494.
XX Novel DNA sequences used to produce modified honey, the metabolites of
XX which can be isolated and purified -

PS Claim 4; Page 26; 56pp; English.
XX The present sequence is that of Petunia hybrida strain W115 FBP15
CC protein, a MADS box protein that is specifically expressed in the
CC nectar of petunia. The sequence was deduced from cDNA (see
CC Z35494 identified by differential expression. The present
CC invention provides a method for producing recombinant proteins in
CC honey. The honey is manufactured by insects, preferably honeybees,
CC that collect the nectar of transgenic plants. The FBP15 gene and
CC its promoter can be utilised in expression cassettes for the
CC production of transgenic plants that produce a protein of interest
CC in their nectar.

XX Sequence 221 AA;

Query Match 57.2%; Score 722; DB 21; Length 221;
Best Local Similarity 64.7%; Pred. No. 9e-63;
Matches 152; Conservative 30; Mismatches 37; Indels 16; Gaps 3;

QY 16 LGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLEYANN 75
Db 1 MGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLEYANN 60
QY 76 SVRGTIERYKKACSDAVNPPSVTEANTOYQOEASKLRQIRDIONSNRHIVGESLSLN 135
Db 61 SVKATIDRYKKASSDSSNTGSTSEANTQYQOEAKLRVQIGNLQNSNRMLGESLSLT 120
QY 136 FKEKLNLEGRLEKISRVRSKKNELLVAEIEYMKRELOHNNMYLRAKIAEGAR-LNP 194
Db 121 AKDLKGLTKLEKIGISRIRSKKNELLFAEIEYMRKREIDLHNNQMLRAKIAESERNVM 180
QY 195 DQESSVIOGTTVYVESGVSHDQSOHYN-RNYIPVNLEPNQOFSQDQPPLOLV 248
Db 181 MGGEFELM-----QSHPYDPRDFQVNGLQHNHQYPRQDNMALQLV 221

RESULT 15
ABG60988
ID ABG60988 standard; Protein; 264 AA.
XX AC ABG60988;
XX DT 27-AUG-2002 (first entry)
DE Novel floral meristem identity protein LpMADS5.

XX Rye grass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS;
KW CEN; CEN-like protein; APETALA2; AP2; AP2-like protein; HB;
KW Homeo-box protein; HB-like protein; plant growth; plant architecture;
KW inflorescence development; flower development; embryo development;
KW seed development; flower organ identity; phase change; male sterility;
KW hybrid seed production; herbage quality; early maturing crop;
KW biomass increase; branching increase; blocking flowering;
KW allergenic pollen; floral meristem identity protein.

XX Lolium perenne.

XX WO200233091-A1.

XX 25-APR-2002.

XX 17-OCT-2001; 2001WO-AU01311.

XX 19-OCT-2000; 2000AU-0000873.

XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

XX (AGRE-) AGRESEARCH LTD.

XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;

XX WPI; 2002-452388/48.

XX N-PSDB; ABK82132.

XX New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases -

XX Claim 16; Fig 91; 290pp; English.

XX The invention describes a substantially purified or isolated polypeptide
CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
CC and HB-like proteins, or their functionally active fragments or variants.
CC Nucleic acid (II) encoding (I), a construct (II) comprising (II), or a
CC vector (IV) comprising (II), is useful for modifying plant life cycles

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 12:42:28 ; Search time 26.1053 Seconds
(without alignments)
1957.448 Million cell updates/sec

Title: US-09-978-382A-4

Perfect score: 1263

Sequence: 1 MEEGGSHDAESSKKLGRGK.....NLLEPNQFGQDPPPLQLV 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1170.5	92.7	249	Q9AXZ1	Q9axz1 brassica na
2	863	68.3	244	Q9YHM3	Q9xhm3 liquidambar
3	854	67.6	249	Q9MBE2	Q9mbe2 rosa rugosa
4	844	66.8	242	Q9VWZ3	Q9vwz3 malus domes
5	837	66.3	225	Q93XH4	Q93xh4 vitis vinif
6	806	63.8	242	Q9LEP2	Q9lep2 betula verr
7	802	63.5	242	Q9ZTV9	Q9ztv9 corylus ave
8	797	63.1	247	Q40900	Q40900 petunia int
9	793	62.8	247	Q08711	Q08711 petunia hyb
10	781.5	61.9	239	Q41195	Q41195 antirrhinum
11	781	61.8	246	Q9ZS29	Q9zs29 gerbera hyb
12	780.5	61.8	246	Q9XFM8	Q9xfm8 antirrhinum
13	780.5	61.8	264	Q9ZS30	Q9zs30 gerbera hyb
14	769.5	60.9	241	Q05111	Q05111 populus tri
15	768	60.8	248	Q41352	Q41352 silene lati
16	766.5	60.7	239	Q48RW5	Q48rw5 phalaenopsi

17	764	60.5	245	10	Q8VWZ2	Q8vwz2 malus domes
18	763.5	60.5	248	10	Q9MBE1	Q9mbe1 rosa rugosa
19	762.5	60.4	248	10	Q9ZRH4	Q9zrh4 rosa hybrid
20	753	59.6	249	10	Q9MBE0	Q9mbe0 rosa rugosa
21	752.5	59.6	250	10	Q9MBD9	Q9mbd9 rosa rugosa
22	745.5	59.0	236	10	Q9ARE9	Q9are9 cucumis sat
23	740	58.6	244	10	Q8RVK1	Q8rvk1 gossypium h
24	739.5	58.6	228	10	Q9ZPK9	Q9zpk9 hyacinthus
25	739.5	58.6	238	10	Q65112	Q65112 populus tri
26	729.5	57.8	253	10	Q42457	Q42457 rumex aceto
27	729	57.7	237	10	Q9SBK1	Q9sbt1 cucumis sat
28	729	57.7	249	10	Q9SBT4	Q9sbt4 fragaria an
29	729	57.7	262	10	Q64958	Q64958 cucumis sat
30	717	56.8	225	10	Q9SBK3	Q9sbk3 cucumis sat
31	705	55.8	221	10	Q9LKQ1	Q9lkl1 cucumis sat
32	705	55.8	229	10	Q64959	Q64959 cucumis sat
33	698.5	55.3	236	10	Q40704	Q40704 oryza sativ
34	698.5	55.3	247	10	Q9AWJ2	Q9awj2 oryza sativ
35	695.5	55.1	254	10	Q43422	Q43422 cucumis sat
36	693	54.9	234	10	Q8RU44	Q8ru44 hordeum vul
37	692	54.8	254	10	Q9SBK2	Q9sbk2 cucumis sat
38	689	54.6	215	10	Q93XE3	Q93xe3 cucumis sat
39	682	54.0	208	10	Q948V3	Q948v3 magnolia pr
40	679	53.8	232	10	Q8RU43	Q8ru43 hordeum vul
41	676.5	53.6	228	10	Q40882	Q40882 petunia hyb
42	670	53.0	259	10	Q24009	Q24009 zea mays (m
43	653.5	51.7	222	10	Q9ZTY6	Q9zty6 pinus resin
44	651.5	51.6	222	10	Q9ZTW4	Q9ztw4 pinus radia
45	649.5	51.4	222	10	Q9ZRC6	Q9zrc6 picea maria

ALIGNMENTS

RESULT 1

Q9AXZ1 ID Q9AXZ1 PRELIMINARY; PRT; 249 AA.
AC Q9AXZ1:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE SHATTERPROOF1.
GN BNSHP1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_taxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BRIDGER;
RA Pylatuik J.D., Davis A.R., Bonham-Smith P.C.;
RT "Molecular cloning and characterization of a B. napus SHP1 gene.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pylatuik J.D., Davis A.R., Bonham-Smith P.C.;
RT "Isolation of the coding region of BnSHP by RT-PCR.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF226865; AAK00646.1; -;
DR EMBL; AY036082; AAK62033.1; -;
DR HSBP; FL1746; IMNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.


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Db 244 TPLQLV 249
|||||
RESULT 4
Q8VWZ3
ID Q8VWZ3 PRELIMINARY; PRT; 242 AA.
AC Q8VWZ3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-type MADS box protein.
GN MADS14.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VEGETATIVE GROWING POINT;
RA van der Linden C.G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=VEGETATIVE GROWING POINT;
RA Vosman B., Smulders M.J.M.;
RT "Isolation of apple B- and C-type MADS box genes from vegetative
RT tissue.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251117; CAC80857.1; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
SQ SEQUENCE 242 AA; 27976 MW; 600B2A3595A37649 CRC64;

Query Match 66.8%; Score 844; DB 10; Length 242;
Best Local Similarity 69.0%; Pred. No. 5.3e-52;
Matches 171; Conservative 31; Mismatches 40; Indels 6; Gaps 3;

QY 1 MEEGSSHDAESSKGLRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60
|| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MEFANQAPESSTQKGLRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVAL 60

QY 61 VIFSTRGLYEYANNSVGTIERYKKACSDAVNPPSVTEANTQYQOEASKLRRIQ 120
|| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 IVFSTRGLYEYANNSVRATIDRYKKACADSTDDGSGVSEANTQYQOEASKLRRIEQ 120

QY 121 NSNRHVGESLGSFKELKNLEGRLEKGISRVSRKKNELLVAIEYMQKREMLQHNMM 180
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 NSNRHILGESLTLKVKELKNLEGRLEKGISRVSRKKNELLFSEIFMQKRETLQHNH 180

QY 181 YLRAKIABGARLNPQOESSVIGQTTVYSGSSHDSOHYNRYIPVNLLPNQOFSGO 240
||||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 FLAKIAESER-EQQQQQTHMIPGTS-YDPSMPNS- ----YDRNFPFVILSNHNHYP 234

QY 241 DQPLQLV 248
| ||||
Db 235 GQATALQLV 242

RESULT 5
Q93XH4
ID Q93XH4 PRELIMINARY; PRT; 225 AA.
AC Q93XH4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
```

```
DE MAD-box transcription factor.
GN MADS1.
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OX NCBI_TaxID=29760;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SHIRAZ; TISSUE=FLOWER, AND FRUIT;
RX MEDLINE=21307190; PubMed=11414613;
RT Boss P.K., Vivier M., Matsumoto S., Dry I.B., Thomas M.R.;
RA "A cDNA from grapevine (Vitis vinifera L.), which shows homology to
RT AGAMOUS and SHATTERPROOF, is not only expressed in flowers but also
RT throughout berry development.";
RL Plant Mol. Biol. 45:541-553(2001).
DR EMBL; AF265562; AAK58564.1; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
SQ SEQUENCE 225 AA; 26151 MW; 509B50DFF92A5503 CRC64;

Query Match 66.3%; Score 837; DB 10; Length 225;
Best Local Similarity 73.0%; Pred. No. 1.5e-51;
Matches 170; Conservative 27; Mismatches 28; Indels 8; Gaps 3;

QY 16 LGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVFTGRGLYEYANN 75
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVFTSRGLYEYANN 60

QY 76 SVRGTIERYKKACSDAVNPPSVTEANTQYQOEASKLRRIQIRDIQNSRHVIGESLGS 135
|| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 SVRTTIERYKKVCSDSNTSGVSEANAGFYQOEASKLRRIQIRDIQNLNRHILGEALUS 120

QY 136 FKELKNLEGRLEKGISRVSRKKNELLVAIEYMQKREMLQHNMYLRAKIABGARLNP 195
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 FKELKNLETRLEKGISRVSRKKNELLFAIEYMQKREIQNSLFLRAQIAENERA--- 177

QY 196 QOESSVIGQTTVYSGSSHDSOHYNRYIPVNLLPNQOFSGOQDPLQLV 248
|| : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 QOQNNLMPGSQ-YE- ----SVPPQPYDSQNLPLVLLDPNNHHYSRHDQATALQLV 225

RESULT 6
Q9LEP2
ID Q9LEP2 PRELIMINARY; PRT; 242 AA.
AC Q9LEP2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MADS box protein.
GN MADS6.
OS Betula verrucosa (White birch) (Betula pendula).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fagales; Betulaceae; Betula.
OX NCBI_TaxID=3505;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FEMALE INFLORESCENCE;
RA Lemmetyinen J., Elo A., Porali I., Sopanen T.;
RT "The ectopic expression of birch genes, BpMADS1 and BpMADS6, causes
RT homeotic changes in the flowers of tobacco and Arabidopsis.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -|- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AJ252071; CAB95649.1; -.
DR HSSP; P11746; 1MNM.
DR InterPro; IPR002487; TF_Kbox.
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DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 242 AA; 27977 MW; CELL2695AEDC5ED6 CRC64;

Query Match 63.8%; Score 806; DB 10; Length 242;
Best Local Similarity 67.2%; Pred. No. 2.5e-49;
Matches 168; Conservative 28; Mismatches 44; Indels 10; Gaps 4;

Qy 1 MEEGGSSHDAESSKGLGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVAL 60
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 61 VIFSTRGRLYEYANN-SVRGTTIERYKKACSDAVNPSPVTEANTQYYQOEASKLRQIRDI 119
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 120 QNSNRHIVGESLGNFKELKLEKIGISRVRSKKNELLVAEIEYMQKREMELOHNN 179
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 180 MYLRAKIAEAGARLNPDQOESSVIOGTTVYESGVSSHDSQHY-NRNYIPVNLLEPNQOFS 238
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 181 QTLRAKIAENER---NQNLNMPGPGNYEL-----MQSQSDSRNRYFQVDALQPNHHYP 232
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 239 GQDQPPLOLV 248
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 233 RQDQIPLQLV 242
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

RESULT 7
Q9ZTV9 PRELIMINARY; PRT; 242 AA.
AC Q9ZTV9;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE MADSL.
GN MADSL.
OS Corylus avellana (European hazel).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fagales; Betulaceae; Corylus.
OX NCBI_TaxID=13451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99084765; PubMed=9869420;
RA Rigola D., Pe M.E., Fabrizio C., Me G., Sari-Gorla M.;
RT "CaMADS1, a MADS box gene expressed in the carpel of hazelnut.";
RL Plant Mol. Biol. 38:1147-1160(1998).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AF027376; AAD03486.1; -.
DR HSSP; P11746; 1MNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00319; SRF-TF; 1.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 2.
DR DNA-binding; Nuclear protein; Transcription regulation.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 242 AA; 28023 MW; 6D74CD865A1B719 CRC64;

Query Match 63.5%; Score 802; DB 10; Length 242;
Best Local Similarity 66.4%; Pred. No. 4.8e-49;
Matches 166; Conservative 31; Mismatches 43; Indels 10; Gaps 4;
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Qy 1 MEEGGSSHDAESSKGLGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVAL 60
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 61 VIFSTRGRLYEYANN-SVRGTTIERYKKACSDAVNPSPVTEANTQYYQOEASKLRQIRDI 119
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 120 QNSNRHIVGESLGNFKELKLEKIGISRVRSKKNELLVAEIEYMQKREMELOHNN 179
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 180 MYLRAKIAEAGARLNPDQOESSVIOGTTVYESGVSSHDSQHY-NRNYIPVNLLEPNQOFS 238
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 181 QTLRAKIAENER---NQNLNMPGPGNYEL-----MQSQSDSRNRYFQVDALQPNHHYP 232
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 239 GQDQPPLOLV 248
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

Qy 233 RQDQIPLQLV 242
Db 1 MEFQNSMSVSPQKLGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEIAL 60

RESULT 8
Q40900 PRELIMINARY; PRT; 247 AA.
AC Q40900;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Agamous protein.
GN PAGLI.
OS Petunia integrifolia (Violet-flowered petunia) (Petunia inflata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PISTIL;
RA Karunanandaa B., Kao T.-h.;
RT "Characterization of a flower-specific cDNA of Petunia inflata
RT encoding a putative homolog of Agamous protein.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: L33973; AAA68001.1; -.
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T03126; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 247 AA; 28389 MW; CIA5F1F0B6E9BECF CRC64;

Query Match 63.1%; Score 797; DB 10; Length 247;
Best Local Similarity 68.6%; Pred. No. 1.1e-48;
Matches 164; Conservative 28; Mismatches 45; Indels 2; Gaps 1;

Qy 10 AESSKKLGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRL 69
Db 11 SSSQKSGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRL 70

Qy 70 YEYANNSVRGTTIERYKKACSDAVNPSPVTEANTQYYQOEASKLRQIRDIQNNSRHVGE 129
Db 71 YEYANNSVRATIDRYKKHHADSTSGSVSEANTQYYQOEAAKLRRQIRDIQTYNRQVGE 130

Qy 130 SLGSLNFKELKLEKIGISRVRSKKNELLVAEIEYMQKREMELOHNNMYLRAKIAEG 189
Db 130 SLGSLNFKELKLEKIGISRVRSKKNELLVAEIEYMQKREMELOHNNMYLRAKIAEG 189
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Db 131 ALSSLPRLKNLEKLEKRAIGVRKKNELLFSEITELMQKRETEMQNANMYLRAKIAEV 190
QY 190 ARLNPDQOESSVIOGTTVYESGVSSHDSOHYNNRNYIPVNLLEPNQOFSQDQPPLOLV 248
Db 191 ERAT--QQMNLMPGGGSEYQQQPMSSSTSQPYDARNFLPVNLLEPNPHYSRODQALQLV 247

RESULT 9
Q08711
ID Q08711 PRELIMINARY; PRT; 247 AA.
AC Q08711.
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Fbp6 protein.
GN FBP6.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W115; TISSUE=CARPEL;
RA Luu J.B.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=W115; TISSUE=CARPEL;
RX MEDLINE=94035167; PubMed=8106081;
RA Angenent G.C., Franken J., Busscher M., Colombo L., van Tunen A.J.;
RT "Petal and stamen formation in petunia is regulated by the homeotic
RT gene fbp1.";
RL Plant J. 4:101-112(1993).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; X68675; CAA48635.1; -.
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T03094; -.
DR InterPro; IPR002487; TF_Kbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00319; SRF-TF; 1.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 247 AA; 28371 MW; 31B7A8D425199DA2 CRC64;

Query Match 62.8%; Score 793; DB 10; Length 247;
Best Local Similarity 68.6%; Pred. No. 2.1e-48;
Matches 164; Conservative 27; Mismatches 46; Indels 2; Gaps 1;

QY 10 AESSKLGKRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGL 69
Db 11 SSSQKSGKRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSSRGL 70

QY 70 YEYANNSVRGTIERYKACSDAVNPPSVTEANTQYQOEAASKLRQRIQNSNRHIVE 129
Db 71 YEYANNSVRATIDRYKKHHADSTSGVSEANTQYQOEAASKLRQRIQTYNRQIVGE 130

QY 130 SGLSNFKELKLEGRLEKISVRSKKNELLVAIEYMQKRELOHNNMYLRAKIAEG 189
Db 131 ALSSLPRLKNLEKLEKRAIGVRKKNELLFSEITELMQKRETEMQNANMYLRAKIAEV 190

QY 190 ARLNPDQOESSVIOGTTVYESGVSSHDSOHYNNRNYIPVNLLEPNQOFSQDQPPLOLV 248
Db 191 ERAT--QQMNLMPGGGSEYQQQPMSSSTSQPYDARNFLPVNLLEPNPHYSRODQALQLV 247

RESULT 10
Q41195
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ID Q41195 PRELIMINARY; PRT; 239 AA.
AC Q41195;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Ple protein.
GN PLE.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93137332; PubMed=8093684;
RA Bradley D., Carpenter R., Sommer H., Hartley N., Coen E.;
RT "Complementary floral homeotic phenotypes result from opposite
RT orientations of a transposon at the plena locus of Antirrhinum.";
RL Cell 72:83-95(1993).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; S53900; AAB25101.1; -.
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T03130; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 239 AA; 27662 MW; D48C6C18043F9682 CRC64;

Query Match 61.9%; Score 781.5; DB 10; Length 239;
Best Local Similarity 65.4%; Pred. No. 1.3e-47;
Matches 159; Conservative 36; Mismatches 39; Indels 9; Gaps 3;

QY 7 SDAESSKLGKRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTR 66
Db 5 NQDSESLKNGKRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSSR 64

QY 67 GRLEYANNSVRGTIERYKACSDAVNPPSVTEANTQYQOEAASKLRQRIQNSNRHI 126
Db 65 GRLEYANNSVRATIERYKACSDAVNPPSVTEANTQYQOEAASKLRQRIQTSNRQM 124

QY 127 VGESLGLNFKELKLEGRLEKISVRSKKNELLVAIEYMQKRELOHNNMYLRAKI 186
Db 125 LGEQVSNMALKDLKSTEAKVEKAIKRSKKNELLFAIEHMQKRELEHNNMFLRAKI 184

QY 187 AEGARLNPDQOESSVIOGTTVYESGVSSHDSOHYNNRNYIPVNLLEPN--QOFSQDQPP 245
Db 185 AEGERA--QQMNLMPGSDYQPMPTSQSYDV----RNELPMNLMEPNQQOYSRHDQ 236

QY 246 QLV 248
Db 237 QLV 239

RESULT 11
Q9ZS29
ID Q9ZS29 PRELIMINARY; PRT; 246 AA.
AC Q9ZS29;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE MADS-box protein, GAGA2.
GN GAGA2.
OS Gerbera hybrida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Mutisiae; Gerbera.
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Job time : 26.1053 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:39:53 ; Search time 9,03644 Seconds
(without alignments)
1138.295 Million cell updates/sec

Title: US-09-978-382a-4
Perfect score: 1263
Sequence: 1 MEEGSSHDAESSKLGK.....NLLEPNQFSGDQPPPLQLV 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1263	100.0	248	1 AGL1_ARATH	P29381 arabidopsis
2	1050	83.1	246	1 AGL5_ARATH	P29385 arabidopsis
3	806.5	63.9	248	1 AG_TOBAC	Q43585 nicotiana t
4	806	63.8	242	1 AG_PANGI	Q40872 panax ginse
5	798.5	63.2	248	1 AG_LYCES	Q40168 lycopersico
6	794.5	62.9	242	1 AG_PETHY	Q40885 petunia hyb
7	752	59.5	252	1 AG_ARATH	P17839 arabidopsis
8	751	59.5	252	1 AG_BRANA	Q01540 brassica na
9	678	53.7	230	1 AGL1_ARATH	Q38836 arabidopsis
10	440.5	34.9	251	1 AGL9_ARATH	Q22456 arabidopsis
11	433	34.3	254	1 AGL9_SINAL	Q04067 sinapis alb
12	430	34.0	241	1 AGL9_PETHY	Q03489 petunia hyb
13	426	33.7	252	1 AGL6_ARATH	P29386 arabidopsis
14	421	33.3	224	1 AGL9_LYCES	Q42454 lycopersico
15	418	33.1	250	1 AGL8_SOLCO	Q40170 lycopersico
16	411.5	32.6	227	1 AGL8_LYCES	Q64645 arabidopsis
17	410.5	32.5	214	1 SOCI_ARATH	Q39685 dianthus ca
18	408.5	32.3	233	1 CMB1_DIAQA	Q38594 aranda debo
19	404.5	32.0	250	1 AGL9_ARADE	P29383 arabidopsis
20	401	31.7	258	1 AGL3_ARATH	Q82743 arabidopsis
21	399.5	31.6	219	1 AGL9_ARATH	P29387 arabidopsis
22	399.5	31.6	244	1 AGL3_ARATH	Q38837 arabidopsis
23	394	31.2	248	1 AGL2_ARATH	P29382 arabidopsis
24	391.5	31.0	250	1 AGL8_SOLCO	Q22328 solanum com
25	391	31.0	254	1 APL_SINAL	Q41276 sinapis alb
26	391	31.0	256	1 APL_ARATH	P35631 arabidopsis
27	382.5	30.3	228	1 AGL1_ARATH	Q9S2j6 arabidopsis
28	381	30.2	242	1 AGL8_ARATH	P38876 arabidopsis
29	378.5	30.0	227	1 AGL7_ARATH	Q38840 arabidopsis
30	378	29.9	250	1 AGL4_ARATH	P29384 arabidopsis
31	377	29.8	241	1 AGL8_SINAL	Q41274 sinapis alb
32	376	29.8	221	1 AGL4_ARATH	Q38838 arabidopsis
33	352	27.9	265	1 JOIN_LYCES	Q9fuy6 lycopersico

34	351	27.8	210	1 FBP1_PETHY	Q03488 petunia hyb
35	345.5	27.4	268	1 AGL5_ARATH	Q38847 arabidopsis
36	343	27.2	211	1 AGL2_ARATH	Q38841 arabidopsis
37	341.5	27.0	264	1 AGL5_BRANA	Q39295 brassica na
38	340.5	27.0	209	1 GLOB_TOBAC	Q03416 nicotiana t
39	339	26.8	240	1 SVP_ARATH	Q9fvc1 arabidopsis
40	332.5	26.3	215	1 GLOB_ANTMA	Q03378 antirrhinum
41	318	25.2	212	1 MAD2_PETHY	Q07474 petunia hyb
42	309	24.5	208	1 PIST_ARATH	P48007 arabidopsis
43	303.5	24.0	232	1 AP3_ARATH	P35632 arabidopsis
44	297.5	23.6	231	1 MAD1_PETHY	Q07472 petunia hyb
45	288.5	22.8	227	1 DEFA_ANTMA	P23706 antirrhinum

ALIGNMENTS

RESULT 1
AGL1_ARATH
ID AGL1_ARATH STANDARD; PRT; 248 AA.
AC P29381;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL1 (Protein Shatterproof 1).
GN AGL1 OR SHP1 OR AT3G58780 OR T20N10_130.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160981; PubMed=1672119;
RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral
homeotic and transcription factor genes.";
RL Genes Dev. 5:484-495(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RC MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoez W., Unseid M.,
FArlmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
Delsen M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
De Simone V., Cholsne N., Artiguenave F., Robert C., Bottier P.,
Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Wiedelmann R., Kranz H., Erfle H., Jordan N., Bangert S.,
Vezi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,
Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordiek G.,
Reichelt J., Scharfe M., Schoen O., Bagues M., Terol J., Climent J.,
Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
Cooke R., Laude M., Berger-Llauro C., Purnelle B., Masuy D.,
de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
Monfort A., Argirou A., Flores M., Liquori R., Vitale D.,
Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Meves H.-W.,
Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
Pai G., Miltscher J., Seilers P., Gill J.E., Feldblyum T.V.,
Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Watanabe A., Yamada M., Yasuda M., Tabata S.;
"Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana".
RL Nature 408:820-822(2000).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-!- SUBCELLULAR LOCATION: Nuclear.

	QY	187	AGARLNPDQES--SVIGTTTYESVSHDSOHNRYNIPVNLLPNCQSGDQPP	244
	Dd	188	AETRAQQOQQOQMNLMPGSSSYELVPPPH--QEDTRNYLQVNGLTNNHHTRDQPS	244
	QY	245	LQLV 248	
	Dd	245	LQLV 248	
	RESULT 4			
	ID	AG_PANGI	STANDARD;	PRT; 242 AA.
	AC	O40872:		
	DT	15-DEC-1998 (Rel. 37, Created)		
	DT	15-DEC-1998 (Rel. 37, Last sequence update)		
	DE	15-JUN-2002 (Rel. 41, Last annotation update)		
	DE	AGAMOUS protein (GAG2).		
	GN	AG2.		
	OS	Panax ginseng (Korean ginseng).		
	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	OC	Asteridae; euasterids II; Apiales; Araliaceae; Panax.		
	OX	NCB1_TaxID=4054;		
	RN	[1]		
	RC	SEQUENCE FROM N.A.		
	RC	TISSUE=Flower;		
	RA	Kim Y.S., Lee H.S., Hoon L.S., Yoo O.J., Chung W.I., Liu J.R.;		
	RT	"The cDNA sequence of two MADS box genes in Panax ginseng (GAG2, GAG1).";		
	RL	(In) Plant Gene Register PGR95-060.		
	CC	-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE FLOWERS (BY SIMILARITY).		
	CC	-!- SUBCELLULAR LOCATION: Nuclear (By similarity).		
	CC	-!- TISSUE SPECIFICITY: FLOWER. PREFERENTIALLY EXPRESSED IN STAMEN AND CARPEL AND WEAKLY IN PETAL. UNDETECTED IN LEAVES AND ROOTS.		
	CC	-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.		
	CC	-!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.		
	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
	DR	EMBL; Z46612; CAA86585.1; --		
	DR	HSP; P11746; LMNM.		
	DR	TRANSFAC; T03099; --		
	DR	InterPro; IPR002487; TF_Kbox.		
	DR	InterPro; IPR002100; TF_MADSbox.		
	DR	Pfam; PF00319; SRF-TF; 1.		
	DR	Pfam; PF01486; K-box; 1.		
	DR	PRINTS; PR00404; MADSDOMAIN.		
	DR	SMART; SM00432; MADS; 1.		
	DR	PROSITE; PS00350; MADS_BOX_1; 1.		
	DR	PROSITE; PS00066; MADS_BOX_2; 1.		
	FT	Transcription regulation; DNA-binding; Activator; Nuclear protein.		
	KW	MADS.		
	FT	DOMAIN 19 73		
	FT	DOMAIN 112 184		
	FT	DOMAIN 194 201		
	FT	DOMAIN 248 AA; 28664 MW; 10BD24A4CB941402 CRC64;		
	SEQ	SEQUENCE		
	Query Match	63.9%; Score 806.5; DB 1; Length 248;		
	Best Local Similarity	65.6%; Pred. No. 4.7e-51;		
	Matches	160; Conservative 36; Mismatches 43; Indels 5; Gaps 2;		
	QY	7	SHAESSKLGRCKIEIKRIENTNRQVTFCRRNGLLKKAYELSLVCDAEVALVFSTR	66
	Dd	8	TREISPKRGLGRCKIEIKRIENTNRQVTFCRRNGLLKKAYELSLVCDAEVALVFSSR	67
	QY	67	GRLEYANNVSVRGTIERYYKKKASDVANPPSVTEANTQYYQAEASKLRQRIRDIQNSNRHI	126
	Dd	68	GRLEYANNVSVKATIERYYKKKASDDSSNTGSISEANAQYYQAEASKLRQINLQNQRNM	127
	QY	127	VGESLGSLNFKEKLNLEGRLEKGISRVRSKNELLVAIEYMOKREMELOHNNMYLRAKI	186
	Dd	128	LGESLAALSURDLKNLEBKTEKISKTRSKNELLFVAIEYMOKRETDLHHNNNOYLRAKI	187

Db	62	IVFSTRGRLEYANNVSKGTTIERKTKACTDSPNTSSSEANAQFQQPASKLRQIISIQ	121	7	SHDAESSKKLGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCAEVALVIFSTR	66
QY	121	NSNRHIVGESLGSFNKLEGRLEKIGISRVRSKKNELLVAEIYEMQKREMELOHNNM	180	8	TRFISPORLGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCAEVALVFSNR	67
Db	122	KNRNMGESLGSFTVRDLKGLTKLEKIGISRVRSKKNELLVAEIYEMQKREMELOHNNM	181	67	GRLEYANNVSKGTTIERKTKACTDSPNTSSSEANAQFQQPASKLRQIISIQ	126
QY	181	YLRAKIAEGARLNPDQESSVIOGTTVYE-SGVSSHDSQHYNNRNPVNLLEPNQOQFSG	239	68	GRLEYANNVSKGTTIERKTKACTDSPNTSSSEANAQFQQPASKLRQIISIQ	127
Db	182	YLRAKIAENARA---QQHNMMPGSSDYELAPPOSFD-----GRNYIQLGLOPNNHYSR	233	127	VRESLSLNFPEKLEKIGISRVRSKKNELLVAEIYEMQKREMELOHNNM	186
QY	240	QDOPPLQLV 248		128	MGEALAGMKLKEKLEGRLEKIGISRVRSKKNELLVAEIYEMQKREMELOHNNM	187
Db	234	QDOPALQLV 242		187	AEAGARLNPDQESSVIOGTTVYEGVSSHDSQHYNNRNPVNLLEPNQOQFSG	242
				188	AETRAQHOHQNMMPG-----SSSNYHELVPVPPQDFTNTYLVQVNGLOQTNNHYPRDQ	242
				243	PPLQLV 248	
				243	PPIQLV 248	
				RESULT 6		
				AG_PETHY		
				ID	AG_PETHY	STANDARD; PRT; 242 AA.
				AC	Q40885;	
				DT	15-DEC-1998 (Rel. 37, Created)	
				DT	15-DEC-1998 (Rel. 37, Last sequence update)	
				DT	15-JUN-2002 (Rel. 41, Last annotation update)	
				DE	AGAMOUS protein (PMADS3).	
				GN	AG1 OR MADS3.	
				OS	Petunia hybrida (Petunia).	
				OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
				OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
				OC	Asteridae; euasterids I; Solanales; Solanaceae; Petunia.	
				OX	NCBI_TaxID=4102;	
				RN	[1]	
				RP	SEQUENCE FROM N.A.	
				RC	TISSUE=Flower;	
				RX	MEDLINE=94004017; PubMed=8104573;	
				RA	Tsuchimoto S., van der Krol A.R., Chua N.H.;	
				RT	"Ectopic expression of PMADS3 in transgenic petunia phenocopies the	
				RT	petunia blind mutant.";	
				RL	Plant Cell 5:843-853(1993).	
				RN	[2]	
				RP	SEQUENCE FROM N.A.	
				RC	STRAIN=cv. Mitchell;	
				RA	Takatsui H., Kapoor M.;	
				RT	"Silencing of PMADS3 affects floral organ and meristem identity in	
				RT	petunia.";	
				RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.	
				CC	-1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING	
				CC	GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE	
				CC	FLOWERS (BY SIMILARITY).	
				CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).	
				CC	-1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN STAMENS AND CARPELS.	
				CC	-1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION	
				CC	FACTORS.	
				CC	-1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.	
				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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				CC	modified and this statement is not removed. Usage by and for commercial	
				CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
				CC	or send an email to license@isb-sib.ch).	
				CC	EMBL; L26295; AAA34197.1; -.	
				DR	HSSP; P11746; 1MNM.	
				DR	TRANSFAC; T03184; -.	
				DR	InterPro; IPR002487; TF_Kbox.	
				DR	InterPro; IPR002100; TF_MADSbox.	
				DR	Pfam; PF00319; SRF-TF; 1.	
				DR	Pfam; PF01486; K-box; 1.	
				DR	PRINTS; PR00404; MADSDOMAIN.	
				DR	SMART; SM00432; MADS; 1.	
				DR	PROSITE; PS00350; MADS_BOX_1; 1.	
				DR	PROSITE; PS00066; MADS_BOX_2; 1.	
				KW	Transcription regulation; DNA-binding; Activator; Nuclear protein.	
				FT	DOMAIN 19 73 MADS.	
				FT	DOMAIN 112 184 K-BOX.	
				SQ	SEQUENCE 248 AA; 28723 MW; E9FDD8DF08ABF1E5 CRC64;	
					Query Match 63.2%; Score 798.5; DB 1; Length 248;	
					Best Local Similarity 65.0%; Pred No. 1.8e-50;	
					Matches 160; Conservative 30; Mismatches 47; Indels 9; Gaps 2;	


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FT DOMAIN 19 73 MADS.
FT DOMAIN 112 184 K-BOX.
FT CONFLICT 1 1 M -> T (IN REF. 1).
SQ SEQUENCE 252 AA; 28723 MW; 4E7591AD85654C1C CRC64;

Query Match 59.5%; Score 752; DB 1; Length 252;
Best Local Similarity 63.2%; Pred. No. 3.8e-47;
Matches 160; Conservative 33; Mismatches 48; Indels 12; Gaps 5;

QY 2 EEGSSHDAESSKKLGRKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVAL 61
Db 6 ELGG---DSSPLRKSGRKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALI 62
QY 62 IFSTRGRLEYANNVSGTIERIYKACSDAVNPSPVTEANTQYQOEASKLRQIRDION 121
Db 63 VFSSRGRLEYNNVSGTIERIYKACSDNTGSAEINAQYQOESAKLRQIISION 122
QY 122 SNRHIVGESLGNFKELNLEGRLEKISVRSKKNELLVAEIMYQKREMELOHNNMY 181
Db 123 SNRQLMGETIGSMFKELNLEGRLEKISVRSKKNELLVAEIMYQKREVDLHNDNQI 182
QY 182 LRAKIAGARLNPDQOESSVITQTTVYESGV-SSHDQSOHY-NRNYIPVNLLEPNQOF-- 237
Db 183 LRAKIAENERNNP---SISLMPGGSNYQLMPPPTQSQPFDSRNYFYVAALQPNHHYS 239
QY 238 --SGODQPPLQLV 248
Db 240 SAGRODQTALQLV 252

RESULT 8
AG_BRANA STANDARD; PRT; 252 AA.
ID AG_BRANA
AC Q01540;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE AGAMOUS protein.
GN AG1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OC NCBI_TaxID=3708;
EN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Westar.
RX MEDLINE=93008236; PubMed=1356631;
RA Mandel M.A., Bowman J.L., Kempin S.A., Ma H., Meyerowitz E.M.,
RA Yanofsky M.F.;
RT "Manipulation of flower structure in transgenic tobacco.";
RL Cell 71:133-143(1992).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
CC FLOWERS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M99415; AAA32985.1; -.
CC PIR; A43484; A43484.
CC HSSP; P11746; 1MNM.
CC TRANSFAC; T01773; -.
CC InterPro; IPR002487; TF_Kbox.
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DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRP-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Activator; Nuclear protein.
FT DOMAIN 19 73 MADS.
FT DOMAIN 112 184 K-BOX.
SQ SEQUENCE 252 AA; 28778 MW; 7C1EF7C96C19EACE CRC64;

Query Match 59.5%; Score 751; DB 1; Length 252;
Best Local Similarity 62.0%; Pred. No. 4.5e-47;
Matches 158; Conservative 34; Mismatches 49; Indels 14; Gaps 5;

QY 1 MEEGSSHDAESSKKLGRKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVAL 60
Db 5 MELGGES---SPQKAGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVAL 61
QY 61 VIFSTRGRLEYANNVSGTIERIYKACSDAVNPSPVTEANTQYQOEASKLRQIRDIO 120
Db 62 IVFSSRGRLEYNNVSGTIERIYKACSDNTGSAEINAQYQOESAKLRQIISIQ 121
QY 121 NSNRHIVGESLGNFKELNLEGRLEKISVRSKKNELLVAEIMYQKREMELOHNNM 180
Db 122 NSNRQLMGETIGSMFKELNLEGRLEKISVRSKKNELLVAEIMYQKREVDLHNDNQ 181
QY 181 YLRAKTAEGARLNPDQOESSVITQTTVYESGVSSHDQSOHY---NRNYIPVNLLEPNQOF 237
Db 182 LLRAKIAENERNNPSPM---SLMPGGSNYEQ-IMPPPTQSQPFDSRNYFYVAALQPNHHH 237
QY 238 ---SGODQPPLQLV 248
Db 238 YSSAGREDQTALQLV 252

RESULT 9
AG11ARATH STANDARD; PRT; 230 AA.
ID AG11ARATH
AC Q38836;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL11.
GN AGL11 OR AT4G09960 OR T5L19.90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Landsberg erecta; TISSUE=Flower;
RX MEDLINE=96004530; PubMed=7549482;
RA Rounsley S.D., Ditta G.S., Yanofsky M.F.;
RT "Diverse roles for MADS box genes in Arabidopsis development.";
RL Plant Cell 7:1259-1269(1995).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone P., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
```



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CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
CC EMBL; M91666; AAA86854.1; -
CC PIR: J01690; J01690.
CC HSSP: P11746; 1MNM.
CC TRANSFAC; T03093; -.
CC InterPro; IPR002487; TF_Kbox.
CC Pfam; PF00319; SRF-TF; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS00666; MADS_BOX_2; 1.
CC Transcription regulation; DNA-binding; Nuclear protein.
CC DOMAIN 3 57 MADS
CC FT DOMAIN 98 170 K-BOX.
CC SEQUENCE 241 AA; 27562 MW; B575BE9468D310BB CRC64;

Query Match 34.0%; Score 430; DB 1; Length 241;
Best Local Similarity 40.4%; Pred. No. 3.8e-24;
Matches 97; Conservative 50; Mismatches 63; Indels 30; Gaps 6;

QY 16 LGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLEYEY-AN 74
Db :|||:||||| :|||:||||| :|||:||||| :|||:||||| :|||:||||| :
1 MGRGRVEMKRIENKINRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLEYEY-AN 60
QY 75 NSVRGTIERVKKA--CSDAVNPPSVTEANTQYQOEASKLRQIRDIQNSNRHIVGESLG 132
Db :|||:||||| :|||:||||| :|||:||||| :|||:||||| :|||:||||| :
61 SSMKLTIERYQK-CNYGAPETNISTREALEISSQYELKUKAYEALQSRNLLGDLG 119
QY 133 SLNFKELKNLEGRLEKGISRVRSKKNELLVAETIYQKREMELOHNNMYLRAKIAEGARL 192
Db |||||:||||| :|||:||||| :|||:||||| :|||:||||| :|||:||||| :
120 PLNSKELESLERLQDMSLKQIRSTRQMLDQDLQKREHALNEANRTLKQRLMEGSTL 179
QY 193 NPQOESESVIOGTTYESGVSHDQSQHNRN-----YIPVNLLEPNQGFSGDQDP 243
Db | :|||:||||| :|||:||||| :|||:||||| :|||:||||| :|||:||||| :
180 NLQWQONA-----QDVGYGRQATQGTGDFHFLPE-CEPTLQIGYQNDP 222

RESULT 13
AGL6_ARATH STANDARD; PRT; 252 AA.
AC P29386;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL6.
GN AGL6 OR AT2G45650 OR F17K2.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN SEQUENCE FROM N.A.
RX MEDLINE=91160981; Pubmed=1672119;
RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral
RT homeotic and transcription factor genes.";
RL Genes Dev. 5:484-495(1991).
```

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OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFNT Cherry; TISSUE=Flower;
RX MEDLINE=93251098; PubMed=1686249;
RA Pnueli L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer Z.,
RA Lifschitz E.;
RT "The MADS box gene family in tomato: temporal expression during
RT floral development, conserved secondary structures and homology with
RT homeotic genes from Antirrhinum and Arabidopsis.";
RL Plant J. 1:255-266(1991).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
CC DEVELOPMENT AND FLORAL ORGANOGENESIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (by similarity).
CC -!- TISSUE SPECIFICITY: FLOWER-SPECIFIC.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC
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CC
CC EMBL; X60758; CAA43170.1; -.
CC EMBL; X60480; CAA43010.1; -.
CC HSSP; P11746; 1MNM.
CC TRANSFAC; T03187; -.
CC InterPro; IPR002487; TF_Kbox.
CC InterPro; IPR002100; TF_MADSbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS00066; MADS_BOX_2; 1.
CC KW Transcription regulation; DNA-binding; Nuclear protein.
CC DOMAIN 3 57 MADS.
CC FT DOMAIN 98 170 K-BOX.
CC SEQUENCE 224 AA; 25999 MW; 51D10D30867D06F7 CRC64;

Query Match 33.3%; Score 421; DB 1; Length 224;
Best Local Similarity 48.1%; Pred. No. 1.5e-23;
Matches 87; Conservative 43; Mismatches 47; Indels 4; Gaps 3;

Qy 16 LGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLYEV-AN 74
Db 1 MGRGVQLKRIENKINQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLYEV-AN 74
:||||:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|
Qy 75 NSVGTITERYKKACSDAVNPPSVT--EANTYQQFASKLRQIRDIQNSRHI 132
Db 61 SSMKLTLEYQK-CNYGAPEPNISTREALISSQQEYLKRGYALQRSQRLNGEDLG 119
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy 133 SLNFELKNLEGRLEKIGTSVRSKKNELLVAEYVMOKREMELOHNNMYLRAKI 192
Db 120 PLNSKELESRLQDMSLKIQIRSTRQLMDQLDQTDYQKREHALNEANRTLKQRLMEGSQL 179
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy 193 N 193
Db 180 N 180

RESULT 15
AGL8_SOLTU STANDARD; PRT; 250 AA.
ID AGL8_SOLTU
AC. Q42429;
```

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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamox-like MADS box protein AGL8 homolog (POTM1-1).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Superior;
RX MEDLINE=96343939; PubMed=8756601;
RA Kang S.G., Hannapel D.J.;
RT "A novel MADS-box gene of potato (Solanum tuberosum L.) expressed
RT during the early stages of tuberization.";
RL Plant Mol. Biol. 31:379-386(1996).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear (by similarity).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC
CC EMBL; U23758; AAA92840.1; -.
CC EMBL; U23757; AAA92839.1; -.
CC HSSP; P11746; 1MNM.
CC TRANSFAC; T03145; -.
CC InterPro; IPR002487; TF_Kbox.
CC InterPro; IPR002100; TF_MADSbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS00066; MADS_BOX_2; 1.
CC KW Transcription regulation; DNA-binding; Nuclear protein.
CC DOMAIN 3 57 MADS.
CC FT DOMAIN 97 169 K-BOX.
CC SEQUENCE 250 AA; 28922 MW; EDE37FFFE793DDC4 CRC64;

Query Match 33.1%; Score 418; DB 1; Length 250;
Best Local Similarity 39.9%; Pred. No. 2.9e-23;
Matches 95; Conservative 46; Mismatches 71; Indels 26; Gaps 6;

Qy 16 LGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLYEV-AN 75
Db 1 MGRGVQLKRIENKINQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLYEV-AN 75
:||||:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|
Qy 76 S-VRGTTIERYKK-----ACSDAVNPPSVTTEANTYQQFASKLRQIRDIQNSRHI 126
Db 61 SCMERLLERYVYSFAERQQLVPTDHTSPGWSWT-----LEHAKLKARLEVLQRNKH 112
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy 127 VGESIGSLNFELKNLEGRLEKIGTSVRSKKNELLVAEYVMOKREMELOHNNMYLRAKI 186
Db 113 VGEDLESINKELNLEQLDLSALKHISRKNQLMHESISVLQKQDRALQEQNNLSKKV 172
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy 187 AEG-----ARLNP-DQOESSVIQGTTVYEGSVSSHDQSOQHYNRNYIPVNLLEPNQOFSG 239
Db 173 KEREKEVAQQNQWDQONHEINSSTFVLPPQL-----DSPHLGEAYQNTNVVDNGEVEG 226
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Search completed: January 27, 2003, 12:44:40
Job time : 10.0364 secs
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:39:53 ; Search time 8.96356 Seconds
(without alignments)
1138.295 Million cell updates/sec

Title: US-09-978-382a-6
Perfect score: 1242
Sequence: 1 MEGGASNEVAESSKKIGRGK.....NLLPNQSSNQDPPLQLV 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1242	100.0	246	1 AGL5_ARATH	P29385 arabidopsis
2	1050	84.5	248	1 AGL1_ARATH	P29381 arabidopsis
3	780.5	62.8	248	1 AG_TOBAC	P43585 nicotiana t
4	772.5	62.2	242	1 AG_PANGI	Q40872 panax ginse
5	770.5	62.0	248	1 AG_LYCES	Q40168 lycopersico
6	767.5	61.8	242	1 AG_PETHY	Q40885 petunia hyb
7	714.5	57.5	252	1 AG_ARATH	P17839 arabidopsis
8	710.5	57.2	252	1 AG_BRANA	Q01540 brassica na
9	704.5	56.7	230	1 AGL1_ARATH	Q38836 arabidopsis
10	427	34.4	252	1 AGL6_ARATH	P29386 arabidopsis
11	411	33.1	214	1 SOCI_ARATH	O64645 arabidopsis
12	407.5	32.8	241	1 AGL9_PETHY	Q03489 petunia hyb
13	405	32.6	250	1 AGL8_SOLTU	Q42429 solanum tub
14	402.5	32.4	248	1 AGL2_ARATH	P29382 arabidopsis
15	401	32.3	224	1 AGL9_LYCES	Q42464 lycopersico
16	401	32.3	233	1 CMBL_DIRCA	Q39685 dianthus ca
17	399.5	32.2	219	1 AGL9_ARATH	O82743 arabidopsis
18	397.5	32.0	250	1 AGL9_ARADE	Q38694 aranda debo
19	396.5	31.9	227	1 AGL8_LYCES	Q42456 arabidopsis
20	394.5	31.8	251	1 AGL9_ARATH	O22456 arabidopsis
21	393.5	31.7	244	1 AGL3_ARATH	P29384 arabidopsis
22	389	31.3	250	1 AGL4_ARATH	P29387 arabidopsis
23	386	31.1	234	1 AGL9_SINAL	O4067 sinapis alb
24	385.5	31.0	258	1 AGL3_ARATH	P29383 arabidopsis
25	383.5	30.9	250	1 AGL8_SOLCO	Q23238 solanum com
26	382	30.8	256	1 APL_ARATH	P35631 arabidopsis
27	378	30.4	242	1 AGL8_ARATH	P38876 arabidopsis
28	377	30.4	241	1 AGL8_SINAL	Q41274 sinapis alb
29	376.5	30.3	254	1 APL_SINAL	Q41276 sinapis alb
30	376	30.3	221	1 AGL4_ARATH	Q38838 arabidopsis
31	372.5	30.0	228	1 AGL1_ARATH	Q9szj6 arabidopsis
32	371	29.9	227	1 AGL7_ARATH	P38840 arabidopsis
33	345	27.8	211	1 AGL2_ARATH	Q38841 arabidopsis

RESULT 1

ID	AGL5_ARATH	STANDARD;	PRT;	246 AA.
AC	P29385; Q9SJH3;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Agamous-like MADS box protein AGL5.			
CN	AGL5 OR AT2G42830 OR F7D19.17.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91160981; PubMed=16721119;			
RA	Ma H., Yanofsky M.F., Meyerowitz E.M.;			
RT	"AGL1-AGL6, an Arabidopsis gene family with similarity to floral			
RT	homeotic and transcription factor genes.";			
RL	Genes Dev. 5:484-495(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=20083487; PubMed=10617197;			
RA	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,			
RA	Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,			
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,			
RA	Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,			
RA	Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,			
RA	Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,			
RA	Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,			
RA	Venter J.C.;			
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis			
RT	thaliana.";			
RL	Nature 402:761-768(1999).			
CC	-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.			
CC	-!- SUBCELLULAR LOCATION: Nuclear.			
CC	-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION			
CC	FACTORS.			
CC	-!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.			
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CC	-----			
DR	EMBL; M55553; AAA32735.1; -.			
DR	EMBL; AC006931; AAD21741.2; -.			
DR	PIR; E39534; E39534.			
DR	HSSP; P11746; LMNM.			
DR	TRANSFAC; T03028; -.			
DR	InterPro: IPR002487; TF_Kbox.			

Q9fvl1 arabidopsis
Q9fuy6 lycopersico
Q38847 arabidopsis
Q39295 brassica na
Q03488 petunia hyb
Q03416 nicotiana t
Q03378 antirrhinum
P48007 arabidopsis
Q07472 petunia hyb
Q07474 petunia hyb
P35632 arabidopsis
P23706 antirrhinum

ALIGNMENTS

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DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 18 MADS.
FT DOMAIN 111 183 K-BOX.
SQ SEQUENCE 246 AA; 28157 MW; D4D59316D55606D9 CRC64;

Query Match 100.0%; Score 1242; DB 1; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.3e-79;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGASNEVAESSKIGRGKTEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60
DB 1 MEGGASNEVAESSKIGRGKTEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60
QY 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTQYYQOEASKLRQIRDIQ 120
DB 61 VIFSTRGRLEYANNVSRGTIERYKKACSDAVNPPTITEANTQYYQOEASKLRQIRDIQ 120
QY 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEYEMQKRETELQNDNM 180
DB 121 NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEYEMQKRETELQNDNM 180
QY 181 YLRSKITERTGLQOQESSVTHQGTVYESGVTSSHQSGQYNNRYIAVNLLPNQNSSNQDQ 240
DB 181 YLRSKITERTGLQOQESSVTHQGTVYESGVTSSHQSGQYNNRYIAVNLLPNQNSSNQDQ 240
QY 241 PPLQLV 246
DB 241 PPLQLV 246

RESULT 2
AGL1_ARATH STANDARD; PRT; 248 AA.
AC P29381;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamou-like MADS box protein AGL1 (Protein Shatterproof 1).
GN AGL1 OR SHP1 OR AT3C58780 OR T20N10.130.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160981; PubMed=1672119;
RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral
RT homeotic and transcription factor genes.";
RN Genes Dev. 5:484-495(1991).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Griuell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
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RESULT 3
AG_TORAC
ID AG_TORAC STANDARD; PRT; 248 AA.
AC Q43585;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE AGAMOUS protein (NAG1).
GN AG1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=cv. Samsun; TISSUP=Stamen;
RX MEDLINE=94120000; PubMed=7507255;
RA Kempin S.A., Mandel M.A., Yanofsky M.F.;
RT "Conversion of perianth into reproductive organs by ectopic
RT expression of the tobacco floral homeotic gene NAG1.";
RL Plant Physiol. 103:1041-1046(1993).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
CC FLOWERS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
CC EMBL; L23925; AAA17033.1; -
CC HSSP; P11746; 1MNM.
CC TRANSFAC; T03106; -
CC InterPro; IPR002487; TF_Kbox.
CC InterPro; IPR002100; TF_MADSbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS00666; MADS_BOX_2; 1.
CC Transcription regulation; DNA-binding; Activator; Nuclear protein.
CC DOMAIN 112 184 K-BOX.
CC DOMAIN 194 201 POLY-GLN.
CC SEQUENCE 248 AA; 28664 MW; 10BD24A4CB941402 CRC64;

Query Match 62.8%; Score 780.5; DB 1; Length 248;
Best Local Similarity 66.9%; Pred. No. 1.3e-47;
Matches 158; Conservative 34; Mismatches 39; Indels 5; Gaps 3;

QY 14 KKGKGIETKRIENTNNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 73
DB 15 RKLGRGKIEIKRIENTNNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 74
QY 74 NNSVGTITERYKKACSDAVNPPTITEANTQYQOEASKLRQIRDTQNLNRHILGESLGS 133
DB 75 NNSVKATIERKKACSDSNSTGSISEANAQYQOEASKLURAIGNLQNRNMLGESLAA 134
QY 134 LNFKELKNLESRLKIGISVRSKKHEMLVAEIEYMQKRETELQNDNMNLRSKI--TERTG 191
DB 135 LSLRLNLEQKIEKIGISKRSKNELLFAEIEYMQKREIDLHNNQYLRAKTAETERAQ 194

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QY 192 LQQQESSV-IHQGTVYESVTSSHSGQYNNRNYIAVNLLEPNQSSNQDPPPLQLV 246
DB 195 QQQQQQNNLMPGSSSYELVPPPHQFD--TRNYLQVNGLTNNHYTRQDQPSQLV 248

RESULT 4
AG_PANGI
ID AG_PANGI STANDARD; PRT; 242 AA.
AC Q40872;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE AGAMOUS protein (GAG2).
GN AG2.
OS Panax ginseng (Korean ginseng).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Araliaceae; Panax.
OX NCBI_TaxID=4054;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Flower;
RA Kim Y.S., Lee H.S., Hoon L.S., Yoo O.J., Chung W.I., Liu J.R.;
RT "The cDNA sequence of two MADS box genes in Panax ginseng (GAG2,
RT GAG1).";
RL (in) Plant Gene Register PGR95-060.
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
CC FLOWERS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: FLOWER. PREFERENTIALLY EXPRESSED IN STAMEN AND
CC CARPEL AND WEAKLY IN PETAL. UNDETECTED IN LEAVES AND ROOTS.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC -----
CC EMBL; Z46612; CAA86585.1; -
CC HSSP; P11746; 1MNM.
CC TRANSFAC; T03099; -
CC InterPro; IPR002487; TF_Kbox.
CC InterPro; IPR002100; TF_MADSbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS00666; MADS_BOX_2; 1.
CC Transcription regulation; DNA-binding; Activator; Nuclear protein.
CC DOMAIN 19 73 MADS.
CC DOMAIN 112 184 K-BOX.
CC SEQUENCE 242 AA; 27781 MW; 0B3F02937B24CF76 CRC64;

Query Match 62.2%; Score 772.5; DB 1; Length 242;
Best Local Similarity 66.1%; Pred. No. 4.7e-47;
Matches 154; Conservative 34; Mismatches 40; Indels 5; Gaps 2;

QY 14 KKGKGIETKRIENTNNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 73
DB 15 RKLGRGKIEIKRIENTNNQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 74
QY 74 NNSVGTITERYKKACSDAVNPPTITEANTQYQOEASKLRQIRDTQNLNRHILGESLGS 133
DB 75 NNSVKATIERKKACTDSPNTSSVSEANAQYQOEASKLRQIEISSIQNNRNMGESLGS 134
QY 134 LNFKELKNLESRLKIGISVRSKKHEMLVAEIEYMQKREIELQNDNMNLRSKITERTGLQ 193

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AG_PETHY	STANDARD;	PRT;	242 AA.
AG_PETHY	STANDARD;	PRT;	242 AA.
Q40885;			
DT	15-DEC-1998 (Rel. 37, Created)		
DT	15-DEC-1998 (Rel. 37, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	AGAMOUS protein (pMADS3).		
AGI	OR MADS3.		
OS	Petunia hybrida (Petunia).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; euasterids I; Solanales; Solanaceae; Petunia.		
OX	NCBI_Taxid=4102;		
RI	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Flower;		
RX	MEDLINE=94004017; PubMed=8104573;		
RA	Tsuchimoto S., van der Krol A.R., Chua N.H.;		
RT	"Ectopic expression of pMADS3 in transgenic petunia phenocopies the		
RL	petunia blind mutant.";		
RL	Plant Cell 5:843-853(1993).		
RP	[2]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Mitchell;		
RA	Takatsuji H., Kapoor M.;		
RT	"Silencing of pMADS3 affects floral organ and meristem identity in		
RL	petunia.";		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING		
CC	GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE		
CC	FLOWERS (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).		
CC	-1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN STAMENS AND CARPELS.		
CC	-1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION		
CC	FACTORS.		
CC	-1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	EMBL; X72912; CAA51417.1; -.		
DR	EMBL; AB076051; BAE79434.1; -.		
DR	HSPSP; P11746; IMNM.		
DR	TRANSFAC; T03135; -.		
DR	InterPro; IPR002487; TF_kbox.		
DR	InterPro; IPR002100; TF_MADSbox.		
DR	Pfam; PF003319; SRF-TF; 1.		
DR	Pfam; PF01486; K-box; 1.		
DR	PRINTS; PR00404; MADSDOMAIN.		
DR	SMART; SM00432; MADS; 1.		
DR	PROSITE; PS00350; MADS_BOX_1; 1.		
DR	PROSITE; PS00066; MADS_BOX_2; 1.		
KW	Transcription regulation; DNA-binding; Activator; Nuclear protein.		
FT	DOMAIN 19 73 MADS.		
FT	112 184		
FT	SEQUENCE 242 AA; 27907 MW; A5249306B807A6BD CRC64;		
SO	K-BOX.		

Query Match 61.8%; Score 767.5; DB 1; Length 242;
 Best Local Similarity 65.7%; Pred. No. 1e-46;
 Matches 153; Conservative 36; Mismatches 39; Indels 5; Gaps 3;

QY 14 KILGRKIKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYEA 73
 DB 15 RKLGRKIKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSSRGRLEYEA 74

QY 74 NNSVRIETRYKACSDAVNPPTITANTOYQOEASKLRQIRDIQNHLHILGESLGS 133
 DB 75 NNSVRIETRYKACSDSNTGSIAGANAQYQOEASKLRQIRDIQNHLHILGESLAA 134

QY 134 LNFKEKLNLESRLKIGSRVRSKHEMLVAIEYMQRETELQNDNMYLRSKITERTGLQ 193
 DB 135 LNDRLNLEQKIEGSKIRAKKNELFAIEYMQRETELQNDNMYLRSKITERTGLQ 192

QY 194 QOESSVHOGTVYESQVTSQSGQVNRNVIANNLLEPNSSNQDQPPQLQV 246
 DB 193 SOOMNLMPPSSSYD--LVPPQOSFD-ARNYLVQNVGLQNNHYPQDQPPQLQV 242

RESULT 7
 AG_ARATH STANDARD; PRT; 252 AA.
 AC PI7839; 082732;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE AGAMOUS protein.
 GN AG OR AT4G18960 OR F13C5.130.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=90309968; PubMed=1973265;
 RA Yanofsky M.F., Ma H., Bowman J.L., Drews G., Feldmann K.A.,
 RA Meyerowitz E.M.;
 RA "The protein encoded by the Arabidopsis homeotic gene agamous
 RT resembles transcription factors";
 RL Nature 346:35-39(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
 RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtheini T.,
 RA Reichert B., Portetle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Billam L., Robben J.,
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzenecker T., Bothé G., Ransperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Borneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Gieles J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
 RA Pettitt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarso A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,

Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 Heifman L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
 Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 Stoneking T., Kallicki J., Graves T., Harmon G., Edwards J.,
 Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 Du H., Ali J., Bernhoff A., Jones K., Drone K., Cotton M., Joshi C.,
 Antonio B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
 Chen E., Marra M., Martienssen R., McCombie W.R.;
 "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:769-777(1999).
 CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
 CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
 CC FLOWERS.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- MISCELLANEOUS: MUTATIONS IN THE AG GENE RESULT IN THE REPLACEMENT
 CC OF THE SIX STAMENS BY SIX PETALS AND OF THE CARPELS BY A NEW
 CC FLOWER.
 CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
 CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC -----
 DR EMBL: X53579; CAA37642.1; ALT INIT.
 DR EMBL: AL021711; CAA16753.1; ALT_SEQ.
 DR EMBL: AL161549; CAB78898.1; ALT_SEQ.
 DR FIR; SI0933; SI0933.
 DR HSP; P11746; IMNM.
 DR TRANSFAC; T01007; .
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF00319; SRF-TF; 1.
 DR Pfam; PF01486; K-Box; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS00666; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein.
 KW TRANSFAC; T01007; .
 FT DOMAIN 19 73 MADS.
 FT DOMAIN 112 184 K-Box.
 FT CONFLICT 1 1 M -> T (IN REF. 1).
 SQ SEQUENCE 252 AA; 28723 MW; 4E7591AD85654C1C CRC64;

Query Match 57.5%; Score 714.5; DB 1; Length 252;
 Best Local Similarity 59.2%; Pred. No. 5.2e-43;
 Matches 148; Conservative 38; Mismatches 53; Indels 11; Gaps 4;

QY 3 GGAASNEVAESSKIGRKIKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVI 62
 DB 8 GGDSSPL-----RKSGRKIKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVI 63

QY 63 FSTRGRLEYANNVSGTTRYKKACSDAVNPPTITANTOYQOEASKLRQIRDIQN 122
 DB 64 FSSRGRLEYANNVSGTTRYKKACSDAVNPPTITANTOYQOEASKLRQIRDIQN 123

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QY 123 NRHLGSLGSLNFKELKNLESLRSGKSKHMLVAEIEYMKRELELQNDNNYL 182
Db 124 NQLMGETIGTSMSPKELNLESLRSGKSKHMLVAEIEYMKRELELQNDNNYL 183
QY 183 RSKITERTGLQOQESSYHOGTVYSGVTSHTSQSGQ--YNNRYIAVNLLEPN---QNSS 236
Db 184 RAKTAENE-RNPFSLMSPGSGNYEQIMPPQOTQOPFDSRNYFOVAALQPNHHYSAG 242
QY 237 NQDQPLQLV 246
Db 243 RQDQALQLV 252

RESULT 8
AG_Brana
ID AG_Brana STANDARD; PRT; 252 AA.
AC Q01540;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE AGAMOUS protein.
GN AG1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Westar;
RX MEDLINE=93008236; PubMed=1356631;
RA Mandel M.A., Bowman J.B., Kempin S.A., Ma H., Meyerowitz E.M.,
RA Yanofsky M.F.;
RT "Manipulation of flower structure in transgenic tobacco.";
RL Cell 71:133-143(1992).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR INVOLVED IN REGULATING
CC GENES THAT DETERMINES STAMEN AND CARPEL DEVELOPMENT IN WILD-TYPE
CC FLOWERS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M99415; AAA32985.1; -
CC PIR; A43484; A43484.
CC HSP; P11746; 1MNM.
CC TRANSFAC; T01773; -
CC InterPro; IPR002487; TF_Kbox.
CC InterPro; IPR002100; TF_MADSbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS00666; MADS_BOX_2; 1.
CC TRANScription regulation; DNA-binding; Activator; Nuclear protein.
CC DOMAIN 19
CC DOMAIN 112
CC DOMAIN 184
CC SEQUENCE 252 AA; 28778 MW; 7C1EF7C96C19EACE CRC64;

Query Match
Best Local Similarity 57.2%; Score 710.5; DB 1; Length 252;
Matches 146; Conservative 39; Mismatches 54; Indels 11; Gaps 4;

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QY 3 GGASNEVAESSKIGRGKTEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVI 62
Db 8 GESS-----PQKAGRGKTEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALVI 63
QY 63 FSTRGRLEYANNVSRGTITERYKKACSDAVNPPTITANTQYQOQESKURRQTRDTONL 122
Db 64 FSSRGRLEYVSNVSGTITERYKKACSDNSNTGSVABINAQYQOQESAKLRQOQIISONS 123
QY 123 NRHLGSLGSLNFKELKNLESLRSGKSKHMLVAEIEYMKRELELQNDNNYL 182
Db 124 NQLMGETIGTSMSPKELNLESLRSGKSKHMLVAEIEYMKRELELQNDNNYL 183
QY 183 RSKITERTGLQOQESSYHOGTVYSGVTSHTSQSGQ--YNNRYIAVNLLEPN---QNSS 236
Db 184 RAKIAENE-RNPFSLMSPGSGNYEQIMPPQOTQOPFDSRNYFOVAALQPNHHYSAG 242
QY 237 NQDQPLQLV 246
Db 243 RQDQALQLV 252

RESULT 9
AG11ARATH
ID AG11ARATH STANDARD; PRT; 230 AA.
AC Q38836;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL11.
GN AGL11 OR AT4G09960 OR TSL19.90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Flower;
RX MEDLINE=96004530; PubMed=7549482;
RA Rounsley S.D., Ditta G.S., Yanofsky M.F.;
RT "Diverse roles for MADS box genes in Arabidopsis development.";
RL Plant Cell 7:1259-1269(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Kieger M., Mueller M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Schmidtkeini T.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtkeini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weijens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzener T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA de Keyser A., Buyshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzl A.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,

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RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latrelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Wil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.,
RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana";
RL Nature 402:769-777(1999).
CC CC
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
CC EMBL; U20182; AAC49080.1; -.
CC EMBL; AL049481; CAB39620.1; -.
CC EMBL; AL161516; CAB78119.1; -.
CC HSP; P11746; INM.
CC TRANSFAC; T03009; -.
CC InterPro; IPR002487; TF_Kbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS50066; MADS_BOX_2; 1.
CC Transcription regulation; DNA-binding; Nuclear protein.
CC DOMAIN 3 57 MADS
CC FT DOMAIN 96 168 K-BOX.
CC SQ SEQUENCE 230 AA; 26183 MW; 336C383355E6CB51 CRC64;

Query Match 56.7%; Score 704.5; DB 1; Length 230;
Best Local Similarity 62.2%; Pred. No. 2.3e-42;
Matches 138; Conservative 33; Mismatches 44; Indels 7; Gaps 1;

QY 16 IGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLRYEYANN 75
Db 1 MGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLRYEYANN 60

QY 76 SVRGTRYKKACSDAVNPPTITEANTQYQOEAASKLRQIRIDIONLRHILGESLGN 135
Db 61 NIRSTERYKKACSDSTNTSTVQINRAYQOESAKLQIQIOTIONSNNLMGDSLSLS 120

QY 136 FKELKNLESLEKGISRVRSKKHEMLVAIEYQKREIELQNDNMVLRSKITERTGLQOQ 195
Db 121 VKELKQVENLEKAIISRKKHLLLEIENAKQREIELQNDNMVLRKVAEVERYQQH 180

QY 196 ESSVIVHQTGYESGVTSQSHSGQGNRYNVIANVLPNNSSN 237
Db 181 HHQMV-----SGSEINATEALASRNYFAHSIMTAGSGSN 215

RESULT 10
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AGL6_ARATH
ID AGL6_ARATH STANDARD; PRT; 252 AA.
AC P29386;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL6.
GN AGL6 OR AT4G45650 OR F17K2.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91160981; PubMed=1672119;
RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral
RL homeotic and transcription factor genes.";
RL Genes Dev. 5:484-495(1991).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RL thaliana.";
RL Nature 402:761-768(1999).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC -----
CC EMBL; M55554; AAA79328.1; -.
CC EMBL; AC003680; AAC06173.1; -.
CC PIR; P39534; F39534.
CC HSP; P11831; ISRS.
CC TRANSFAC; T03029; -.
CC InterPro; IPR002487; TF_Kbox.
CC InterPro; IPR002100; TF_MADSbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS50066; MADS_BOX_2; 1.
CC Transcription regulation; DNA-binding; Nuclear protein.
CC DOMAIN 3 57 MADS
CC FT DOMAIN 95 167 K-BOX.
CC SQ SEQUENCE 252 AA; 28744 MW; F763A4A71515CF20 CRC64;

Query Match 34.4%; Score 427; DB 1; Length 252;
Best Local Similarity 42.7%; Pred. No. 4.5e-23;
Matches 100; Conservative 42; Mismatches 74; Indels 18; Gaps 6;

QY 16 IGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLRYEYANN 75
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Db 1 MGRGRVEMKRIENKINQVTFSKRRNGLLKAYELSVLCDAEVALIFSSRGKLYEFGSV 60
QY 76 SVRGTIERYKKA--CSDAVNPPTITEANTQYQOEASKLRQIRDIQNLNHLGSLGS 133
Db 61 GIESTIERYNRCYNSLNNKP---EETQSWCQEVTKLSKSYSLVTRNLLGDLGE 117
QY 134 LNFKELKNLESRLKGISRVRSKKHMLVAEIEYMKREIELQNDNMVLRSKITERTGLQ 193
Db 118 MGKVEQLAERLEAALATQRKQTYVMMEEDLRKQRLGDLNKLKIF-ETEG-- 174
QY 194 QOESSVHQGTVEGVTSSHQSG--GOYNNRYIAVNLLEPNQSSNQDPPQLQ 245
Db 175 -----HAKFTQDLWANSASVAGDPNNSEFPVPSHPNVLDON-TEPFIQI 220

RESULT 11
ID SOC1_ARATH STANDARD; PRT; 214 AA.
AC 064645;
DT 15-JUN-2002 (Rel. 41, Created)
DE 15-JUN-2002 (Rel. 41, Last sequence update)
DE SUPPRESSOR OF CONSTANS OVEREXPRESSION 1 protein (Agamous-like MADS box protein AGL20).
GN SOC1 OR AGL20 OR AT2G45660 OR F17K2.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=20571356; PubMed=11123798;
RA Borner R., Kampmann G., Chandler J., Gleissner R., Wisman E., Apel K.,
RA Melzer S.;
RT "A MADS domain gene involved in the transition to flowering in Arabidopsids."
RL Plant J. 24:591-599(2000).
RN 2;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana."
RL Nature 402:761-768(1999).
RN 3;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RTKEN Arabidopsis full length cDNA clones (RAFTs) sequenced by the SSP consortium (Salk/Stanford/PGEC)."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN 4;
RP FUNCTION.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=20450897; PubMed=10995392;
RA Lee H., Suh S.S., Park E., Cho E., Ahn J.H., Kim S.G., Lee J.S.,
RA Kwon Y.M., Lee I.;
RT "The AGAMOUS-LIKE 20 MADS domain protein integrates floral inductive pathways in Arabidopsis."
RL Genes Dev. 14:2366-2376(2000).
CC -!- FUNCTION: Probable transcription factor active in flowering time control. May integrate signals from the photoperiod, vernalization and autonomous floral induction pathways.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
```

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RP SEQUENCE FROM N.A.
RX MEDLINE=93005737; PubMed=1356537;
RA Angenent G.C., Busscher M., Franken J., Mol J.N.M., van Tunen A.J.;
RT "Differential expression of two MADS box genes in wild-type and
FT mutant petunia flowers.";
RL Plant Cell 4:983-993(1992).
RN [2]
RP REVISIONS TO C-TERMINUS.
RA Angenent G.C.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
DR EMBL; M91666; AAA86854.1; -
DR PIR; JQ1690; JQ1690.
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T03093; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRP-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 98 170 K-BOX.
SQ SEQUENCE 241 AA; 27562 MW; B575BE9468D310BB CRC64;

Query Match 32.8%; Score 407.5; DB 1; Length 241;
Best Local Similarity 43.3%; Pred. No. 9.6e-22;
Matches 91; Conservative 48; Mismatches 62; Indels 9; Gaps 5;

QY 16 IGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLRYEY-AN 74
Db :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
1 MGRGRVELKRIENKINQVTFKRRNGLLKAYELSVLCDAEVALVIFSTRGLRYEFCSS 60
QY 75 NSVRGTIERYKKACSDAVNPPTIT--EANTQYQOEASKLRQIRDIQNLRHILGESLG 132
Db :||:||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
61 SSMILKTLERYQK-CNYGAPETNISTREALTSSQOEYLLKARYEALQRSQRLNGEDLG 119
QY 133 SLNFKELKNLESLEKGISRVRSKKHEMLVARIEMVKREIELONDNMVLRSKITERT-- 190
Db |||||:||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
120 PLNSKELESLEQLDMSLKQIRSTRFTQLMDLQDLQRKEHALNEANRTLKORLMEGSTL 179
QY 191 GLOQESSVTHQGTVEGSGVTSSHQSGOYN 220
Db |||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
180 NLQWQNA---QDVGYGRQATQTQGDGFPH 206

RESULT 13
AGL8_SOLTU
ID AGL8_SOLTU STANDARD; PRT; 250 AA.
AC Q42429;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, last sequence update)
DE Agamous-like MADS box protein AGL8 homolog (POTM1-1).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxId=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Superior;
RX MEDLINE=96343939; PubMed=8756601;
RA Kang S.G., Hannapel D.J.;
RT "A novel MADS-box gene of potato (Solanum tuberosum L.) expressed
RT during the early stages of tuberization.";
RL Plant Mol. Biol. 31:379-386(1996).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
DR EMBL; U23758; AAA92840.1; -
DR EMBL; U23757; AAA92839.1; -
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T03145; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRP-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 97 169 K-BOX.
SQ SEQUENCE 250 AA; 28922 MW; EDE37FFFE793DDC4 CRC64;

Query Match 32.6%; Score 405; DB 1; Length 250;
Best Local Similarity 39.3%; Pred. No. 1.5e-21;
Matches 94; Conservative 47; Mismatches 74; Indels 24; Gaps 6;

QY 16 IGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGLRYEYANN 75
Db :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
1 MGRGRVQLKRIENKINQVTFCKRRSGLLKKAHEISVLCDAEVLIVFSTRGLKFAYAND 60
QY 76 S-VRGTIERYKK-----ACSDAVNPPTITTEANTQYQOEASKLRQIRDIQNLRHI 126
Db ||: |||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
61 SCMERLLERYYSFAERQLVPTDFTSPGSWT-----LEHAKLKARLEVLRQNRHY 112
QY 127 LGESLGLSNFKELKNLESLEKGISRVRSKKHEMLVARIEMVKREIELONDNMVLRSKI 186
Db :|||:||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
113 VGEDLESNNKELQNLQHEQLDSALKHTRSKRNQNMHESISVLQKQDRALQONNLSKKV 172
QY 187 TERTG-LQQ----QESSVTHQGT-VYESGVTSHQSGOYNRYIANVLLPEPNQSSNQ 238
Db |||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
173 KEREKVAQONQOWDOQHNEINSFTFVLPOQLDSPHLGEAYQNTNVVDNGEYEGGSSQ 231

RESULT 14
AGL2_ARATH
ID AGL2_ARATH STANDARD; PRT; 248 AA.
AC P29382;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, last sequence update)
DE Agamous-like MADS box protein AGL2.
DE Agamous-like MADS box protein AGL2.
GN AGL2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:42:53 ; Search time 14.4413 Seconds
(without alignments)
1637.600 Million cell updates/sec

Title: US-09-978-382A-6
Perfect score: 1242
Sequence: 1 MEGASNEVAESSKKIGRKG.....NLLEPNQNSSNQDPPPLQLV 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1242	100.0	246	2	E39534	floral homeotic pr
2	1238	99.7	258	2	G84858	floral homeodomain
3	1050	84.5	248	2	A39534	floral homeotic pr
4	780.5	62.8	248	2	T03592	floral homeotic pr
5	771	62.1	247	2	S60307	fbp6 protein - gar
6	770.5	62.0	248	2	T07185	floral homeotic pr
7	767.5	61.8	242	2	JQ2212	pMADS3 protein - g
8	742.5	59.8	239	2	A44343	promotes sex organ
9	714.5	57.5	284	2	T05033	floral homeotic pr
10	714.5	57.5	284	2	A85214	floral homeotic pr
11	710.5	57.2	252	2	A43494	probable transcrip
12	710	57.2	229	2	T08040	MADS-box protein -
13	709	57.1	262	2	T08039	MADS-box protein -
14	705.5	56.8	254	2	T10185	MADS-box protein C
15	704.5	56.7	230	2	T04000	MADS-box protein A
16	700.5	56.4	236	2	S59480	MADS-box protein 3
17	695.5	56.0	253	2	S57586	MADS-box regulator
18	656	52.8	259	2	T01700	hypothetical prote
19	647	52.1	286	2	JQ2289	floral homeotic pr
20	646.5	52.1	222	2	S51934	MADS-box protein d
21	629.5	50.7	265	2	T02261	MADS box protein -
22	587	47.3	258	2	PQ0770	floral homeotic pr
23	481	38.7	261	2	S51935	probable MADS-box
24	479	38.6	261	2	T09603	MADS-box protein 3
25	451.5	36.4	242	2	T10486	MADS box protein -
26	449.5	36.2	242	2	T09571	MADS box protein M
27	448.5	36.1	250	2	T04167	MADS box protein -
28	443	35.7	255	2	T03408	MADS box protein -
29	436	35.1	255	2	T03398	MADS box protein -

30	427	34.4	252	2	F39534	floral homeotic pr
31	421	33.9	273	2	T03410	MADS box protein -
32	420	33.8	219	2	S46526	MADS box protein m
33	418	33.7	221	2	T10751	MADS-box protein M
34	417.5	33.6	245	2	T09569	MADS box protein M
35	415.5	33.5	213	2	T10432	MADS box protein A
36	411	33.1	214	2	T00879	MADS-box protein A
37	409	32.9	248	2	T04170	MADS-box protein A
38	407	32.8	203	2	S51936	MADS-box protein d
39	406	32.7	224	2	JQ1690	MADS box protein f
40	406	32.7	225	2	T04168	MADS box protein -
41	405.5	32.6	249	2	T04307	M79 protein - rice
42	405.5	32.6	249	2	T04335	MADS box protein -
43	405	32.6	250	2	T07100	MADS box protein h
44	405	32.6	257	2	S53306	MADS box protein M
45	404	32.5	246	2	T17023	MADS box protein 1

ALIGNMENTS

RESULT 1

E39534
floral homeotic protein AGL5 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999
C:Accession: E39534
R:Ma, H.; Yanofsky, M.F.; Meyerowitz, E.M.
Genes Dev. 5, 484-495, 1991
A:Title: AGL1-AGL6, an Arabidopsis gene family with similarity to floral homeotic and
A:Reference number: A39534; MUID:91160981; PMID:1672119
A:Accession: E39534
A:Molecule type: DNA
A:Residues: 1-246 <MAA>

A:Cross-references: GB:M55553; NID:g166595; PIDN:AAA32735.1; PID:g166596
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C:Keywords: DNA binding; nucleus; transcription regulation
F:17-72/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 100.0%; Score 1242; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 3.6e-79;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEGGASNEVAESSKKIGRKGIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL	60
Db	1	MEGGASNEVAESSKKIGRKGIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVAL	60
Qy	61	VIFSTRGRLYEYANNSVRGTIERYKKACSDAVNPPTITEANTOYYQGFASKLRQIRDIQ	120
Db	61	VIFSTRGRLYEYANNSVRGTIERYKKACSDAVNPPTITEANTOYYQGFASKLRQIRDIQ	120
Qy	121	NLNRRILGESLSNPKELKNLESLEKISRVRSKKHEMLVAIEYMQKREIELQNDNM	180
Db	121	NLNRRILGESLSNPKELKNLESLEKISRVRSKKHEMLVAIEYMQKREIELQNDNM	180
Qy	181	YLRSKITERTGLQOQESSVHOGTVYESGVTSOSHSGOYNRYTAVNLLPEPNQSSNODQ	240
Db	181	YLRSKITERTGLQOQESSVHOGTVYESGVTSOSHSGOYNRYTAVNLLPEPNQSSNODQ	240
Qy	241	PPLQLV 246	
Db	241	PPLQLV 246	

RESULT 2

G84858
floral homeodomain transcription factor (AGL5) [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: G84858
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: G84858

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-258 <STO>

A:Cross-references: GB:AE002093; NID:g4512687; PIDN:AAD21741.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g42830

A:Map position: 2

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

Query Match 99.7%; Score 1238; DB 2; Length 258;

Best Local Similarity 100.0%; Pred. No. 7.2e-79;

Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGASNEVAESSKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60

Db 1 MEGASNEVAESSKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLEYANNVSGTIERYKKACSDAVNPPTITEANTYYQOEASKLRRIIDIQ 120

Db 61 VIFSTRGRLEYANNVSGTIERYKKACSDAVNPPTITEANTYYQOEASKLRRIIDIQ 120

QY 121 NLNRHILGESLGNFKELKNLESRLKESISRSVRSKHKHEMLVAEYMKREIELQNDNM 180

Db 121 NLNRHILGESLGNFKELKNLESRLKESISRSVRSKHKHEMLVAEYMKREIELQNDNM 180

QY 181 YLRSKITERTGLOQESSVIHQGTVYESGVTSSSHQSGQYNNRYIAVNLEPNQNSNQDQ 240

Db 181 YLRSKITERTGLOQESSVIHQGTVYESGVTSSSHQSGQYNNRYIAVNLEPNQNSNQDQ 240

QY 241 PPLQL 245

Db 241 PPLQL 245

RESULT 3

A39534

floral homeotic protein AGL1 [similarity] - Arabidopsis thaliana

N:Alternate names: agamous-like 1 AGL1; Shatterproof 1 SHPI; T20N10.130

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jun-2000

C:Accession: A39534; T49161

R:Ma, H.; Yanofsky, M.F.; Meyerowitz, E.M.

Genes Dev. 5, 484-495, 1991

A:Title: AGL1-AGL6, an Arabidopsis gene family with similarity to floral homeotic and tr

A:Reference number: A39534; MUID:91160981; PMID:1672119

A:Accession: A39534

A:Molecule type: DNA

A:Residues: 1-248 <MAA>

A:Cross-references: GB:M55550; NID:g166587; PIDN:AAA32730.1; PID:g166588

R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; I

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z25017

A:Accession: T49161

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-248 <DAN>

A:Cross-references: EMBL:AL353032; GSPDB:GN00061; ATSP:T20N10.130

A:Experimental source: cultivar Columbia; BAC clone T20N10

C:Genetics:

A:Gene: ATSP:T20N10.130

A:Map position: 3

A:Introns: 76/2; 103/3; 124/2; 157/3; 171/3; 185/3

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C:Keywords: DNA binding; nucleus; transcription regulation

F:17-72/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 84.5%; Score 1050; DB 2; Length 248;

Best Local Similarity 85.5%; Pred. No. 7.5e-66;

Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

QY 1 MEGASNEVAESSKIGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60

Db 1 MEGGSHDAESSKLGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVAL 60

QY 61 VIFSTRGRLEYANNVSGTIERYKKACSDAVNPPTITEANTYYQOEASKLRRIIDIQ 120

Db 61 VIFSTRGRLEYANNVSGTIERYKKACSDAVNPPTITEANTYYQOEASKLRRIIDIQ 120

QY 121 NLNRHILGESLGNFKELKNLESRLKESISRSVRSKHKHEMLVAEYMKREIELQNDNM 180

Db 121 NSNRHIVGESLGNFKELKNLEGRLEKISRSVRSKKNELLVAEYMQREMLQNNM 180

QY 181 YLRSKITE--RTGLOQESSVIHQGTVYESGVTSSSHQSGQYNNRYIAVNLEPNQNSNQ 238

Db 181 YLRKIAEAGARLNPDQESSVIQGTIVYESGVSHDQSHYNNRYIPVNLEPNQFSGQ 240

QY 239 DQPPLQLV 246

Db 241 DQPPLQLV 248

RESULT 4

T03592

floral homeotic protein NAG1 - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Sep-1999

C:Accession: T03592

R:Kempin, S.A.; Mandel, M.A.; Yanofsky, M.F.

Plant Physiol. 103, 1041-1046, 1993

A:Title: Conversion of perianth into reproductive organs by ectopic expression of the

A:Reference number: Z14965; MUID:94120000; PMID:7507255

A:Accession: T03592

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-248 <KEM>

A:Cross-references: EMBL:L23925; NID:g431735; PIDN:AAAL7033.1; PID:g431736

A:Experimental source: cultivar Samsun; tissue-type immature stamens

C:Genetics:

A:Gene: NAG1

C:Function:

A:Description: NAG1 seems to be sufficient to convert perianth into reproductive flor

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho

C:Keywords: DNA binding; nucleus; transcription regulation

F:18-73/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 62.8%; Score 780.5; DB 2; Length 248;

Best Local Similarity 66.9%; Pred. No. 3.7e-47;

Matches 158; Conservative 34; Mismatches 39; Indels 5; Gaps 3;

QY 14 KKTGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLEYA 73

Db 15 RKLGRGKIEIKRIENTTNRQVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLEYA 74

QY 74 NNSVGRGTYRKKACSDAVNPPTITEANTYYQOEASKLRRIQIDIONLNRHILGESLGS 133

Db 75 NNSVKATIERYKKACSDSSNTGSISEANAQYYQOEASKLRQIGNLQNNRNWLGESLAA 134

QY 134 LNFKELKNLESRLKESISRSVRSKHKHEMLVAEYMKREIELQNDNMVLRSKI--TERTG 191

Db 135 LSLURLANLEQKIEKGISKIRSKKNELLFAEYMKREIDLHNNNNQYLRAKIAETERAQ 194

QY 192 LQQOESSV-IHQGTVYESGVTSSSHQSGQYNNRYIAVNLEPNQNSNQDQPPLQLV 246

Db 195 QQQQQQNNLMPGSSSYELVPPPHQFD--TRNYLQVNGLQNNHNTROPDQPLQLV 248

RESULT 5

S60307

fbp6 protein - garden petunia

C:Species: Petunia x hybrida (garden petunia)

C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 24-Sep-1999

C:Accession: S60307

[illegible]


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      8 GCESS-----PQKAGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALIV 63
      63 FSTRGRLEYEYANNVSGTTERYKACSDAVNPPTITANTQYYQOQASKLRRQIRDIQNL 122
      64 FSSRGRLEYEYNNVSGTTERYKKAISDNTSGVAEINQAQYYQOQASAKLRQIISIQNS 123
      123 NRHILGESLGNFKELKNLESRLKISVRSKKHEMLVAEIEYMKRELELQNDNYL 182
      124 NQLMGETIGSMSPKELNLEGLRDSVNRIRSKKNELLFAEIDYMKREVDLHNDQLL 183
      183 RKTERTGLQOQESSVHHQGTVYESGVTSSSHQSQ--YRNRYIAVNLLLEPN----QNSS 236
      184 RAKIAENE--RNNPSMLMPGGSNYEQIMPQPQTPQPPQDFSKRYFOVAALQPNHHYSAG 242
      237 NQDQPPQLQIV 246
      243 REDQTALQIV 252

RESULT 12
T08040
MADS-box protein - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C:Accession: T08040
R:Kater, M.M.; Colombo, L.; Franken, J.; Busscher, M.; Masiero, S.; van Lookeren Campagne
Plant Cell 10, 171-182, 1998
A:Title: Multiple AGAMOUS homologs from cucumber and petunia differ in their ability to
A:Reference number: Z16308; MUID:98158685; PMID:9490741
A:Accession: T08040
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-229 <KAT>
A:Cross-references: EMBL:AF035439; NID:g2997614; PIDN:AAC08529.1; PID:g2997615
C:Genetics:
A:Gene: CUM10
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 57.2%; Score 710; DB 2; Length 229;
Best Local Similarity 59.9%; Pred. No. 2.6e-42;
Matches 145; Conservative 41; Mismatches 30; Indels 26; Gaps 4;

QY 16 IGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALIVFSTRGRLEYEYANN 75
Db 1 MGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALIVFSSRGRLEYEYNN 60

QY 76 SVRGTIERYKKACSDAVNPPTITANTQYYQOQASKLRRQIRDIQNLN---RHILGESL 131
Db 61 SIKTTIERYKKACSDSSATSSVTELNTQYYQOQASAKLRQIQIQLNLSNVLVRHLMGDSL 120

QY 132 GSLNFKELKNLESRLKISVRSKKHEMLVAEIEYMKRELELQNDNYLRSKITERGTG 191
Db 121 SALATYKELQLENLERGITRIRSKKHEMLLABIEYLOKREIELEENVCVTRTKIAEVER 180

QY 192 LQO-----QESSVTHQGTVYESGVTSSSHQSQGYNNRYIAVNLLLEP--NONSSNQDQPP 243
Db 181 VQQANWVGQELNALI-----QALANSRNFFSPNIMEPAGVPVSYSHQDKML 226

QY 244 QL 245
Db 227 HL 228

RESULT 13
T08039
MADS-box protein - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C:Accession: T08039
R:Kater, M.M.; Colombo, L.; Franken, J.; Busscher, M.; Masiero, S.; van Lookeren Campagne

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Plant Cell 10, 171-182, 1998
A:Title: Multiple AGAMOUS homologs from cucumber and petunia differ in their ability
A:Reference number: Z16308; MUID:98158685; PMID:9490741
A:Accession: T08039
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-262 <KAT>
A:Cross-references: EMBL:AF035438; NID:g2997612; PIDN:AAC08528.1; PID:g2997613
C:Genetics:
A:Gene: CUM1
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C:Keywords: DNA binding; nucleus; transcription regulation
F:43-98/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 57.1%; Score 709; DB 2; Length 262;
Best Local Similarity 63.7%; Pred. No. 3.6e-42;
Matches 149; Conservative 32; Mismatches 41; Indels 12; Gaps 3;

QY 14 KKICRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALIVFSTRGRLEYEY 73
Db 40 RKMGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALIVFSSRGRLEYEY 99

QY 74 NNSVRGTIERYKKACSDAVNPPTITANTQYYQOQASKLRRQIRDIQNLNRHILGESLGS 133
Db 100 NNSVKATIDRYKKACSDSSNTGSTSEANTQYYQOQAAKLRVQIGNLQNSNRNRMIGESLSS 159

QY 134 LNFPELKNLESRLKISVRSKKHEMLVAEIEYMKREIELELQNDNYLRSKITERGTGLQ 193
Db 160 LTAQDLKLGLETKLEKIGSIRSKKNELLFAEIEYMKREIDLHNNQMLRAKIAE----- 214

QY 194 QOESSVTHQGTVYESGVTSSSHQSQGYN--RNYIAVNLLLEPNQNSNQDQPPQLQIV 246
Db 215 -SERNVNMMGGEF-----LMQSHPYDPRDFQVNGLQHNHOYPRQDNMALQIV 262

RESULT 14
T10185
MADS-box protein CUS1 - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C:Accession: T10185
R:Filipecki, M.K.; Sommer, H.; Malepszy, S.
Plant Sci. 125, 63-74, 1997
A:Title: The MADS-box gene CUS1 is expressed during cucumber somatic embryogenesis.
A:Reference number: Z16982
A:Accession: T10185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-254 <FIL>
A:Cross-references: EMBL:X97801; NID:g1321796
A:Experimental source: cv. Borszczagowski; developmental stage: somatic embryogenesis
C:Genetics:
A:Gene: cus1
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C:Keywords: DNA binding; transcription factor; transcription regulation
F:26-81/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 56.8%; Score 705.5; DB 2; Length 254;
Best Local Similarity 61.4%; Pred. No. 6e-42;
Matches 140; Conservative 35; Mismatches 50; Indels 3; Gaps 1;

QY 10 AESSKKIGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALIVFSTRGRL 69
Db 19 SSSSRGTGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALIVFSSRGR 78

QY 70 YEYANNSVRGTIERYKKACSDAVNPPTITANTQYYQOQASKLRRQIRDIQNLNRHILGE 129
Db 79 YEYANNSVRATISRYKKAYSDPSTAMTVSEANTQYYQOQASAKLRQIQLNLRHLLGE 138

QY 130 SLGSLNFKELKNLESRLKISVRSKKHEMLVAEIEYMKREIELELQNDNYLRSKITER 189
Db 139 SSSLSVKDLKSLVKLEKIGSIRSKKNELLFSEIEYMKREIELEHTNQLIRAKIAET 198

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:44:48 ; Search time 8.46559 Seconds
(without alignments)
586.365 Million cell updates/sec

Title: US-09-978-382A-6

Perfect score: 1242

Sequence: 1 MEGASNEVAESSKKIGRKG.....NLLEPNQSSNQDPPIQLIV 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap:*
7: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1242	100.0	246	9	US-09-978-729A-6
2	1242	100.0	246	9	US-09-981-087A-6
3	1242	100.0	246	9	US-09-978-382A-6
4	1242	100.0	246	9	US-09-978-740A-6
5	1242	100.0	246	10	US-09-978-730-6
6	1050	84.5	248	9	US-09-978-729A-4
7	1050	84.5	248	9	US-09-981-087A-4
8	1050	84.5	248	9	US-09-978-382A-4
9	1050	84.5	248	9	US-09-978-740A-4
10	1050	84.5	248	10	US-09-978-730-4
11	421	33.9	273	9	US-09-853-450-8
12	417	33.6	240	10	US-09-970-624-2
13	411	33.1	214	9	US-09-853-450-34
14	402.5	32.4	248	9	US-09-853-450-28
15	397.5	32.0	251	9	US-09-853-450-12
16	397	32.0	255	9	US-09-853-450-10
17	389	31.3	250	9	US-09-853-450-30
18	382	30.8	256	9	US-09-853-450-2
19	378	30.4	242	9	US-09-978-729A-2

20	378	30.4	242	9	US-09-981-087A-2	Sequence 2, Appli
21	378	30.4	242	9	US-09-978-382A-2	Sequence 2, Appli
22	378	30.4	242	9	US-09-978-740A-2	Sequence 2, Appli
23	378	30.4	242	10	US-09-978-730-2	Sequence 2, Appli
24	378	30.4	253	9	US-09-853-450-4	Sequence 4, Appli
25	376	30.3	255	9	US-09-853-450-6	Sequence 6, Appli
26	374.5	30.2	237	9	US-09-853-450-32	Sequence 32, Appli
27	348.5	28.1	220	9	US-09-853-450-38	Sequence 38, Appli
28	336.5	27.1	150	9	US-09-853-450-14	Sequence 14, Appli
29	322	25.9	210	9	US-09-853-450-26	Sequence 36, Appli
30	268.5	21.6	173	9	US-09-853-450-40	Sequence 40, Appli
31	248	20.0	105	10	US-09-767-215-10	Sequence 10, Appli
32	244.5	19.7	192	9	US-09-853-450-50	Sequence 50, Appli
33	216	17.4	507	10	US-09-876-187-2	Sequence 2, Appli
34	216	17.4	507	10	US-09-749-728B-13	Sequence 13, Appli
35	213	17.1	465	10	US-09-749-728B-17	Sequence 17, Appli
36	213	17.1	473	10	US-09-876-187-6	Sequence 6, Appli
37	213	17.1	473	10	US-09-876-187-8	Sequence 8, Appli
38	209	16.8	365	10	US-09-876-187-4	Sequence 4, Appli
39	209	16.8	365	10	US-09-749-728B-15	Sequence 15, Appli
40	202.5	16.3	521	10	US-09-749-728B-19	Sequence 19, Appli
41	198.5	16.0	676	10	US-09-801-368-302	Sequence 302, App
42	197.5	15.9	286	10	US-09-801-368-188	Sequence 188, App
43	159	12.8	452	10	US-09-801-368-336	Sequence 336, App
44	97.5	7.9	374	10	US-09-925-302-711	Sequence 711, App
45	95.5	7.7	697	10	US-09-815-242-12798	Sequence 12798, A

ALIGNMENTS

RESULT 1

US-09-978-729A-6

; Sequence 6, Application US/09978729A

; Patent No. US20020178465A1

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

; APPLICANT: Liljgren, Sarah

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 19452A-000950US

; CURRENT APPLICATION NUMBER: US/09/978,729A

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: US 60/090,649

; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: US 09/339,998

; PRIOR FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 246

; TYPE: PRT

; ORGANISM: Arabidopsis sp.

US-09-978-729A-6

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Best Local Similarity 100.0%; Pred. No. 2.8e-99;

Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	121	NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIELQNDNM	180
Db	121	NLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIELQNDNM	180
Qy	181	YLRSKITERTGLQQQESSVIHQCTVYESGVTSSHOSQYNNFYIAVNLLEPNQSSNQDO	240

Qy	121	NLNRRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQKREIELQNDNM	180
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Qy	181	YLRSKITERTGLQQOESSVIHOGTVYESGVTSSHQSGQYNNRTIAVNLLFPNQNSSNODQ	240
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Qy	241	PPLQLV 246	
Db	241	PPLQLV 246	
RESULT 5			
US-09-978-730-6			
; Sequence 6, Application US/09978730			
; Patent No. US20020129403A1			
; GENERAL INFORMATION:			
; APPLICANT: Yanofsky, Martin F.			
; APPLICANT: Liljegen, Sarah			
; TITLE OF INVENTION: The Regents of the University of California			
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic			
; FILE REFERENCE: 19452A-0009200S			
; CURRENT APPLICATION NUMBER: US/09/978,730			
; CURRENT FILING DATE: 2001-10-15			
; PRIOR APPLICATION NUMBER: US 60/090,649			
; PRIOR FILING DATE: 1998-06-25			
; PRIOR APPLICATION NUMBER: US 09/339,998			
; PRIOR FILING DATE: 1999-06-25			
; NUMBER OF SEQ ID NOS: 25			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 6			
; LENGTH: 246			
; TYPE: PRT			
; ORGANISM: Arabidopsis sp.			
; SS-09-978-730-6			

Query Match	100.0%;	Score 1242;	DB 10;	Length 246;
Best Local Similarity	100.0%;	Pred. No. 2.8e-99;		
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QY	61	VIFSTRGRLYEYANNSVRGTTIERYKKACSDAVNPPTTTEANTQYYQQBASKLRQIRDIQ	120
DB	61	VIFSTRGRLYEYANNSVRGTTIERYKKACSDAVNPPTTTEANTQYYQQBASKLRQIRDIQ	120
QY	121	NLNRHILGESLGSNLFRELKKNLESRLKGISRVRSKHEMLVAETYMOKREIELQNDNM	180
DB	121	NLNRHILGESLGSNLFRELKKNLESRLKGISRVRSKHEMLVAETYMOKREIELQNDNM	180
QY	181	YLRSKITERTGLQOOESSV IHOGTVYSGVTS SHQSGQYNNRYIAVNLLPNQNSSNODQ	240
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QY	241	PPQLQV 246	
DB	241	PPQLQV 246	

RESULT 6

US-09-978-729A-4

; Sequence 4, Application US/09978729A

; Patent No. US20020178465A1

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

; APPLICANT: Liljegen, Sarah

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic Plants

; TITLE OF INVENTION: Plants

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; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978,729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-729A-4

Query Match      84.5%; Score 1050; DB 9; Length 248;
Best Local Similarity 85.5%; Pred. No. 7.7e-81;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

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QY      61 VIFSTRGLXEYANNSVRGTIERYKKACSDAVNPPTITEANTYYQOEASKLRROIRDIQ 120
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QY      181 YLRSKITE--RTGLQQOESSVYHOGTVYESGVTSSHSGOYNRYIAVNLLEPNONSSNQ 238
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QY      239 DOPPLQLV 246
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DB      241 DOPPLQLV 248
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RESULT 7
US-09-981-087A-4
; Sequence 4, Application US/09981087A
; Patent No. US20020178466A1
; GENERAL INFORMATION:
; APPLICANT: Ianoofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: Fariandiz, Cristina
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000940US
; CURRENT APPLICATION NUMBER: US/09/981,087A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-981-087A-4

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Query Match	84.5%	Score 1050;	DB 9;	Length 248;
Best Local Similarity	85.5%;	Pred. No. 7.7e-83;		
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Db 121 NSNRHIVGESLGNFKELKNLESRLKIGISRVRSKKHEMLVAETIYQOEASKLRROIRDIQ 180
QY 181 YLRSKITE--RTGLQQOESSVTHOQTIVYSGVTSQSHSQGNRNRYIAVNLLEPNQNSNQ 238
Db 181 YLRAKIAEGARLNPDOQESSVTHOQTIVYSGVTSQSHSQGNRNRYIPVNLLEPNQNSNQ 240
QY 239 DOPPLQLV 246
Db 241 DOPPLQLV 248

RESULT 8
US-09-978-382A-4
; Sequence 4, Application US/09978382A
; Publication No. US20020194647A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000930US
; CURRENT FILING DATE: 2002-06-18
; PRIOR FILING DATE: 1998-06-25
; PRIOR FILING DATE: 1998-06-25
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-382A-4
Query Match 84.5%; Score 1050; DB 9; Length 248;
Best Local Similarity 85.5%; Pred. No. 7.7e-83;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;

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Db 181 YLRAKIAEGARLNPDOQESSVTHOQTIVYSGVTSQSHSQGNRNRYIPVNLLEPNQNSNQ 240
QY 239 DOPPLQLV 246
Db 241 DOPPLQLV 248

RESULT 9
US-09-978-740A-4
; Sequence 4, Application US/09978740A
; Publication No. US20030005481A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000920US
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 1998-06-25
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-740A-4
Query Match 84.5%; Score 1050; DB 10; Length 248;
Best Local Similarity 85.5%; Pred. No. 7.7e-83;
Matches 212; Conservative 12; Mismatches 22; Indels 2; Gaps 1;
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 12:39:28 ; Search time 31.3725 Seconds
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Sequence: 1 MEGGASNEVAESSKKIGRCK.....NLEPNQNSSNQDPPLQLV 246

Scoring table: BLOSUM62
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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	746.5	60.1	241	22	Amino acid sequenc
8	746.5	60.1	241	23	Poplar floral home
9	719.5	57.9	238	21	Arabidopsis thalia
10	719.5	57.9	238	22	Amino acid sequenc

11	719.5	57.9	238	23	ABG30868	Poplar floral home
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15	704.5	56.7	230	21	AAAG16690	Arabidopsis thalia
16	704.5	56.7	230	21	AAAG40213	Arabidopsis thalia
17	702	56.5	221	21	AAAY58648	Petunia nectary-sp
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19	698	55.2	185	21	AAAB32638	Eucalyptus grandis
20	690.5	55.6	264	23	ABG60988	Novel floral meris
21	680	54.8	257	21	AAAG33135	Zea mays protein f
22	680	54.8	260	21	AAAG33134	Zea mays protein f
23	680	54.8	283	21	AAAG33133	Zea mays protein f
24	676	54.4	268	23	ABG60931	Novel floral meris
25	673	54.2	133	21	AAAG07156	Arabidopsis thalia
26	658.5	53.0	229	17	AAAR9637	Eucalyptus AGE-2 p
27	648.5	52.2	222	21	AAAB26795	Plant reproductive
28	630	50.7	268	21	AAAG43856	Zea mays protein f
29	539	43.4	161	21	AAAB33229	Eucalyptus grandis
30	522	42.0	122	21	AAAG33756	Arabidopsis thalia
31	503	40.5	142	21	AAAG12611	Zea mays protein f
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33	479	38.6	261	19	AAAW48623	Pinus radiata cone
34	462.5	37.2	260	23	ABG60946	Novel floral meris
35	449.5	36.2	181	21	AAAB33310	Pinus radiata tran
36	449.5	36.2	242	19	AAAW48622	Pinus radiata cone
37	448.5	36.1	250	21	AAAL7679	Plant flowering ti
38	444	35.7	281	21	AAAG29741	Arabidopsis thalia
39	443.5	35.7	205	23	ABG60922	Novel floral meris
40	429	34.5	240	21	AAAY96767	Z. mays MADS-box p
41	428.5	34.5	250	20	AAW84048	Rice OSMAD56 prote
42	427	34.4	252	21	AAAG29742	Arabidopsis thalia
43	425	34.2	270	22	AAAB68357	Amino acid sequenc
44	424	34.1	228	23	ABG60925	Novel floral meris
45	424	34.1	245	23	ABG60944	Novel floral meris

ALIGNMENTS

RESULT 1
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ID AAW81000 standard; Protein; 246 AA.
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AC AAW81000;
XX
DT 10-MAY-1999 (first entry)
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DE Arabidopsis AGL5 polypeptide.
XX
KW AGL5-like gene; agamous-like 5 gene; seed dispersal; dehiscence;
KW transgenic plant.
XX
OS Arabidopsis thaliana.
XX
PN WO9900502-Al.
XX
PD 07-JAN-1999.
XX
PF 25-JUN-1998; 98WO-US13208.
PR 28-APR-1998; 98US-0067800.
PR 27-JUN-1997; 97US-0051030.
XX (REGC) UNIV CALIFORNIA.
XX Ferrandiz C, Yancofsky MF;
XX WPI: 1999-095747/08.
DR N-PSDB; AAY99858, AAY99860.
XX
XX Use of agamous-like nucleic acids - useful for the production of
transgenic seed plants in which dehiscence is modified resulting in

PR 16-JUL-1999;	99US-0144086.	PR 08-OCT-1999;	99US-0158232.
PR 19-JUL-1999;	99US-0144325.	PR 12-OCT-1999;	99US-0158369.
PR 19-JUL-1999;	99US-0144331.	PR 13-OCT-1999;	99US-0159293.
PR 19-JUL-1999;	99US-0144332.	PR 13-OCT-1999;	99US-0159294.
PR 19-JUL-1999;	99US-0144333.	PR 13-OCT-1999;	99US-0159295.
PR 19-JUL-1999;	99US-0144334.	PR 14-OCT-1999;	99US-0159329.
PR 19-JUL-1999;	99US-0144335.	PR 14-OCT-1999;	99US-0159330.
PR 20-JUL-1999;	99US-0144352.	PR 14-OCT-1999;	99US-0159331.
PR 20-JUL-1999;	99US-0144632.	PR 14-OCT-1999;	99US-0159637.
PR 20-JUL-1999;	99US-0144684.	PR 18-OCT-1999;	99US-0159638.
PR 21-JUL-1999;	99US-0144814.	PR 18-OCT-1999;	99US-0159584.
PR 21-JUL-1999;	99US-0145086.	PR 21-OCT-1999;	99US-0160741.
PR 21-JUL-1999;	99US-0145088.	PR 21-OCT-1999;	99US-0160767.
PR 22-JUL-1999;	99US-0145085.	PR 21-OCT-1999;	99US-0160768.
PR 22-JUL-1999;	99US-0145087.	PR 21-OCT-1999;	99US-0160770.
PR 22-JUL-1999;	99US-0145089.	PR 21-OCT-1999;	99US-0160814.
PR 22-JUL-1999;	99US-0145192.	PR 21-OCT-1999;	99US-0160815.
PR 23-JUL-1999;	99US-0145145.	PR 22-OCT-1999;	99US-0160980.
PR 23-JUL-1999;	99US-0145218.	PR 22-OCT-1999;	99US-0160981.
PR 23-JUL-1999;	99US-0145224.	PR 22-OCT-1999;	99US-0160989.
PR 26-JUL-1999;	99US-0145276.	PR 25-OCT-1999;	99US-0161404.
PR 27-JUL-1999;	99US-0145913.	PR 25-OCT-1999;	99US-0161405.
PR 27-JUL-1999;	99US-0145918.	PR 25-OCT-1999;	99US-0161406.
PR 27-JUL-1999;	99US-0145919.	PR 26-OCT-1999;	99US-0161359.
PR 28-JUL-1999;	99US-0145951.	PR 26-OCT-1999;	99US-0161360.
PR 02-AUG-1999;	99US-0146386.	PR 26-OCT-1999;	99US-0161361.
PR 02-AUG-1999;	99US-0146388.	PR 28-OCT-1999;	99US-0161920.
PR 02-AUG-1999;	99US-0146389.	PR 28-OCT-1999;	99US-0161920.
PR 03-AUG-1999;	99US-0147038.	PR 28-OCT-1999;	99US-0161992.
PR 04-AUG-1999;	99US-0147204.	PR 28-OCT-1999;	99US-0161993.
PR 04-AUG-1999;	99US-0147302.	PR 29-OCT-1999;	99US-0162142.
PR 05-AUG-1999;	99US-0147192.		
PR 05-AUG-1999;	99US-0147260.		
PR 06-AUG-1999;	99US-0147303.		
PR 06-AUG-1999;	99US-0147416.		
PR 09-AUG-1999;	99US-0147493.		
PR 09-AUG-1999;	99US-0147935.		
PR 10-AUG-1999;	99US-0148171.		
PR 11-AUG-1999;	99US-0148319.		
PR 12-AUG-1999;	99US-0148341.		
PR 13-AUG-1999;	99US-0148565.		
PR 13-AUG-1999;	99US-0148684.		
PR 16-AUG-1999;	99US-0149368.		
PR 17-AUG-1999;	99US-0149175.		
PR 18-AUG-1999;	99US-0149426.		
PR 20-AUG-1999;	99US-0149722.		
PR 20-AUG-1999;	99US-0149723.		
PR 20-AUG-1999;	99US-0149929.		
PR 23-AUG-1999;	99US-0149902.		
PR 23-AUG-1999;	99US-0149930.		
PR 25-AUG-1999;	99US-0150566.		
PR 26-AUG-1999;	99US-0150884.		
PR 27-AUG-1999;	99US-0151065.		
PR 27-AUG-1999;	99US-0151066.		
PR 27-AUG-1999;	99US-0151080.		
PR 30-AUG-1999;	99US-0151303.		
PR 31-AUG-1999;	99US-0151438.		
PR 01-SEP-1999;	99US-0151930.		
PR 07-SEP-1999;	99US-0152363.		
PR 10-SEP-1999;	99US-0153070.		
PR 13-SEP-1999;	99US-0153758.		
PR 15-SEP-1999;	99US-0154018.		
PR 16-SEP-1999;	99US-0154039.		
PR 20-SEP-1999;	99US-0154779.		
PR 22-SEP-1999;	99US-0155139.		
PR 23-SEP-1999;	99US-0155486.		
PR 24-SEP-1999;	99US-0155659.		
PR 28-SEP-1999;	99US-0156458.		
PR 29-SEP-1999;	99US-0156596.		
PR 04-OCT-1999;	99US-0157117.		
PR 05-OCT-1999;	99US-0157753.		
PR 06-OCT-1999;	99US-0157865.		
PR 07-OCT-1999;	99US-0158029.		
Query Match 99.7%; Score 1238; DB 21; Length 258;			
Best Local Similarity 100.0%; Pred. No. 4.7e-113;			
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1	MEGASNEVAESSKIGRGKIEIKRIENTTNROVTECKRRNGLLKAYELSVLCDAEVAL 60		
DB 1	MEGASNEVAESSKIGRGKIEIKRIENTTNROVTECKRRNGLLKAYELSVLCDAEVAL 60		
QY 61	VIFSTRGRLYEYANNVSRGTIERYKKACSDAVNPPTITEANTQYYQQEASKLRRIQDIQ 120		
DB 61	VIFSTRGRLYEYANNVSRGTIERYKKACSDAVNPPTITEANTQYYQQEASKLRRIQDIQ 120		
QY 121	NLNRHILGESLGSINPKELKNLESRLKGSIRVRSKKHEMLVAETIYMQKREIELQNDNM 180		
DB 121	NLNRHILGESLGSINPKELKNLESRLKGSIRVRSKKHEMLVAETIYMQKREIELQNDNM 180		
QY 181	YLRSKITERTGLQQQESSVIHQGTVYESGVTSSHQSGOYNRNYIAVNLLPQNSSNQDQ 240		
DB 181	YLRSKITERTGLQQQESSVIHQGTVYESGVTSSHQSGOYNRNYIAVNLLPQNSSNQDQ 240		
QY 241	PPLQL 245		
DB 241	PPLQL 245		
RESULT 3			
AAW80999			
ID	AAW80999 standard; Protein; 248 AA.		
XX			
AC	AAW80999;		
XX			
XX			
DT	10-MAY-1999 (first entry)		
XX			
DE	Arabidopsis AGL1 polypeptide.		
XX			
KW	AGL1-like gene; agamous-like 1 gene; seed dispersal; dehiscence;		
XX	transgenic plant.		
OS	Arabidopsis thaliana.		
XX			
PN	W09900502-A1.		
XX			

AAR99633	233	-ONSSNQDQPLQLV	246
ID	AAR99633	standard; Protein; 251 AA.	
XX	AC		
XX	AC		
XX	AAR99633;		
DT	01-OCT-1996	(first entry)	
XX	DE		
XX	DE	Eucalyptus AGE-1 protein.	
XX	KW	Eucalyptus; reproductive gene; AGE1; Arabidopsis; agomous gene;	
KW	KW	Antirrhinum; plena gene; sterility; fertility; forest tree;	
KW	KW	transgenic plant; flower development; antisense; ribozyme.	
XX	OS	Eucalyptus globulus.	
XX	Key	Location/Qualifiers	
XX	Region	18..73	
FT	FT	/label= MADS_box	
XX	XX		
PN	AU9539013-A.		
XX	PD		
XX	30-MAY-1996.		
XX	XX		
XX	22-NOV-1995;	95AU-0039013.	
XX	XX		
XX	22-NOV-1994;	94AU-0009589.	
XX	XX		
XX	PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
XX	XX		
XX	PI	Dennis ES, Harcourt RL, Kyoza J, Llewellyn D;	
XX	PI	Peacock WJ, Southerton S;	
XX	XX		
DR	WPI; 1996-278411/29.		
DR	N-PSDB; AAT34428.		
XX	XX		
XX	PT	Eucalyptus reproductive genes - useful for prodn. of sterile	
XX	PT	Eucalyptus trees useful for establishing wood lot plantations or in	
XX	PT	re-forestation projects	
XX	PS	Disclosure; Page 29-30; 60pp; English.	
XX	XX		
XX	CC	AGE-1 protein (AAR99633) is the product of a cDNA clone, AGE1	
XX	CC	(AAT34428), isolated from Eucalyptus globulus cDNA on the basis of	
XX	CC	its homology to the Arabidopsis agamous (AG) and Antirrhinum plena	
XX	CC	(PLE) flower development genes. AGE-1 shows 68% homology to AG and	
XX	CC	75% homology to PLE protein. AGE1 is very highly expressed in	
XX	CC	mature flower buds. A related protein, AGE-2 (AAR99637), was also	
XX	CC	identified. Antisense or ribozyme constructs of AGE, or of FLE2 and	
XX	CC	SQE genes (see also AAT34426 and AAT34429-31), can be used to produce	
XX	CC	sterile transgenic Eucalyptus trees by minimising inflorescence.	
XX	SQ	Sequence 251 AA;	
Query Match 66.4%; Score 824.5; DB 17; Length 251;			
Best Local Similarity 68.6%; Pred. No. 1.7e-72;			
Matches 175; Conservative 26; Mismatches 41; Indels 13; Gaps 5;			
QY	1	MEGASNAVEASSKKI-CRGKTEIKRIENTTNQVTECKRRNGLLKAYELSVLCDAEVA	59
DB	1	MEFPSEFSEASSQKRGGRGKTEIKRIENTTNQVTECKRRNGLLKAYELSVLCDAEVA	60
QY	60	LVIPTSGRLYEYANNSVRGTTIERYKKACSDAVNPPTITEANTQYQOQASKLRQIRDI	119
DB	61	LIVFSSRGLYEYANNSVRGTTIERYKKACSDSSHPQSVSEVNTQFYQOQASKLRQIREI	120
QY	120	QNLNHIILGESLGSUNFELKLNLESLEKISGRVRSKKHEMLVAEIEYMQKRIELONDN	179
DB	121	QVSNRHIILGEGISDLSFKDLNLESKLEKISGRVRSKKHEMLFAEIEYMQKRIELOND	180
QY	180	MYLRSKI--TERTGLQOQESSVIH-----QGTVYSGVTSSSHSGOYNRYIAVNLLPN	232
DB	181	MYLRKAIENERAQQOQQGSDHFNMPGSSSVYE-----ALPSQPAYDRNFLQVNVLEPN	236

QY	233	-ONSSNQDQPLQLV	246
DB	237	HQSYRSRSDHTALQLV	251
RESULT 6			
ID	AAV58656	standard; Protein; 241 AA.	
XX	AC		
XX	AC	AAV58656;	
DT	11-APR-2000	(first entry)	
XX	DE	Poplar PTAG-1 floral homeotic gene-encoded protein.	
XX	KW	Poplar; PTAG-1; floral homeotic gene; transgenic plant; sterility;	
KW	KW	fertility.	
XX	OS	Populus balsamifera subsp. trichocarpa.	
XX	Key	Location/Qualifiers	
XX	Domain	17..33	
FT	FT	/note= "MADS domain"	
FT	FT	106..172	
FT	FT	/note= "K domain"	
XX	XX		
PN	CA2227940-A1.		
XX	XX		
XX	PD	06-OCT-1999.	
XX	XX		
XX	07-APR-1998;	98CA-2227940.	
XX	XX		
XX	06-APR-1998;	98US-0080851.	
XX	XX		
XX	PA	(UYOR-) UNIV OREGON HEALTH SCI.	
XX	XX		
XX	PI	Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;	
XX	XX		
DR	WPI; 2000-1066662/10.		
DR	N-PSDB; AA257946, AA257947.		
XX	XX		
XX	PT	Nucleic acid from Populus trichocarpa genes, useful for producing	
XX	PT	transgenic plants, particularly trees, with modified fertility	
XX	XX	characteristics such as sterility -	
XX	PS	Claim 31; Page 67-68; 92pp; English.	
XX	XX		
XX	CC	The present sequence is that of the novel PTAG-1 protein of poplar	
XX	CC	(Populus balsamifera subsp. trichocarpa), as deduced from newly	
XX	CC	isolated gene and cDNA sequences (see AA257946-47). PTAG-1 is 1	
XX	CC	of 4 novel floral homeotic genes identified in this poplar species.	
XX	CC	It is a homologue of AGAMOUS and is expressed in floral tissues.	
XX	CC	PTAG-1 contains a MADS domain and a K-domain. The invention	
XX	CC	provides nucleic acid sequences of the 4 novel Populus genes, the	
XX	CC	corresponding cDNA sequences (see AA247942-49) and deduced amino acid	
XX	CC	gene and cDNA sequences to produce genetically engineered Populus	
XX	CC	and other trees having modified fertility characteristics, including	
XX	CC	sterility. Genetic constructs useful in producing genetically	
XX	CC	engineered Populus and other trees include antisense versions of	
XX	CC	PTAG-1, dominant negative mutants, and constructs useful for sense	
XX	CC	suppression. Sterile trees allow increased wood yield and a	
XX	CC	reduction in the production of allergens such as pollen.	
XX	SQ	Sequence 241 AA;	
Query Match 60.1%; Score 746.5; DB 21; Length 241;			
Best Local Similarity 63.2%; Pred. No. 7.1e-65;			
Matches 153; Conservative 41; Mismatches 41; Indels 7; Gaps 3;			
QY	7	NEVAESS--KKIGRGKIEIKRIENTTNQVTECKRRNGLLKAYELSVLCDAEVALVIFS	64
DB	5	NESLESSPLRLGRGKVEIKRIENTTNQVTECKRRRGLLKAYELSVLCDAEVALIFS	64

XX PS Disclosure; Column 67-70; 46pp; English.

XX CC The invention relates to an isolated nucleic acid molecule especially a

CC protein transduction domain (PTD) promoter: (i) that hybridises under

CC wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 %SDS (sodium

CC dodecyl sulphate) at 65 plusC to nucleotides or (ii) comprising 35

CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic

CC gene and is the homologue of DEFICIENS. Also includes are a recombinant

CC nucleic acid comprising the PTD promoter, a cell transformed with

CC the recombinant nucleic acid and a transgenic plant comprising the

CC transformed cell. The PTD promoter is useful to obtain floral-specific

CC expression of genes such as cytotoxins, that are employed in genetic

CC ablation strategies to produce trees having modified fertility

CC characteristics, including sterility. Genetic constructs comprising

CC antisense versions or dominant negative mutants of PTD are useful in

CC producing genetically engineered Poplars and other trees, and for sense

CC suppression. Also disclosed are 3 other homeotic genes PTLF, PTAG-1

CC and PTAG-2 (none are defined). The present sequence is the PTAG-1

CC protein.

XX Sequence 241 AA;

Query Match 60.1%; Score 746.5; DB 23; Length 241;

Best Local Similarity 63.2%; Pred. No. 7.1e-65;

Matches 153; Conservative 41; Mismatches 41; Indels 7; Gaps 3;

QY 7 NEVAESS--KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFS 64

Db 5 NESLESSPLRLKGRGKVEIKRIENTTNQVTFCKRRSGLLKAYELSVLCDAEVALVIFS 64

QY 65 TRGLYEYANNSVGTIERYKKACSDAVNPPTITTEANTYYQOEASKLRQRDIQNLSNR 124

Db 65 SRGLYEYNSVSTIERYKKACSDSSNTGSVSEANAQYYQOEAAKLRSQIGNLSNR 124

QY 125 HILGESLGLNFKEKLNLESLEKGISRVSRKKHEMLVAEIEYMKREIEIQNDNMVLS 184

Db 125 HMLGEALSSLVKELKLEIRLEKGISRSKKNELLFAEIEYMKREYDVLHNNQLLRA 184

QY 185 KITERTGLOQESSVIHOGTVYESGVTSSHSGOYNRYIAVNLLPEPNQSSNQDPPLO 244

Db 185 KISENE-RKROSMNMLPGGADFEIVQSPYDS----RNYSQVNGLPASHYSHQDQMALQ 239

QY 245 LV 246

Db 240 LV 241

RESULT 9

AAV58657

ID AAV58657 standard; Protein; 238 AA.

XX AC AAV58657;

XX DT 11-APR-2000 (first entry)

XX DE Poplar PTAG-2 floral homeotic gene-encoded protein.

XX KW Poplar; PTAG-2; floral homeotic gene; transgenic plant; sterility;

XX KW fertility.

XX OS Populus balsamifera subsp. trichocarpa.

XX FH Key Location/Qualifiers

FT Domain 17..33

FT /note= "MADS domain"

FT Domain 106..172

FT /note= "K domain"

XX CA2227940-A1.

XX PD 06-OCT-1999.

XX

PF 07-APR-1998; 98CA-2227940.

XX 06-APR-1998; 98US-0080851.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;

PI WPI: 2000-106662/10.

DR N-PSDB; AAZ57848, AAZ57949.

XX Nucleic acid from Populus trichocarpa genes, useful for producing

PT transgenic plants, particularly trees, with modified fertility

PT characteristics such as sterility -

XX Claim 31; Page 77; 92pp; English.

XX The present sequence is that of the novel PTAG-2 protein of poplar

CC (Populus balsamifera subsp. trichocarpa), as deduced from newly

CC isolated gene and cDNA sequences (see AAZ57948-49). PTAG-2 is 1

CC of 4 novel floral homeotic genes identified in this poplar species.

CC It is a homologue of AGAMOUS and is expressed in floral tissues.

CC PTAG-2 contains a MADS domain and a K-domain. The invention

CC provides nucleic acid sequences of the 4 novel Populus genes, the

CC corresponding cDNA sequences (see AAZ47942-49) and deduced amino acid

CC sequences (see AAY58454-57). It also provides methods of using the

CC gene and cDNA sequences to produce genetically engineered Populus

CC and other trees having modified fertility characteristics, including

CC sterility. Genetic constructs useful in producing genetically

CC engineered Populus and other trees include antisense versions of

CC PTAG-2, dominant negative mutants, and constructs useful for sense

CC suppression. Sterile trees allow increased wood yield and a

CC reduction in the production of allergens such as pollen.

XX Sequence 238 AA;

Query Match 57.9%; Score 719.5; DB 21; Length 238;

Best Local Similarity 62.3%; Pred. No. 3.1e-62;

Matches 147; Conservative 39; Mismatches 43; Indels 7; Gaps 3;

QY 7 NEVAESS--KKIGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFS 64

Db 5 NEQESSPRLKGRGKVEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIFS 64

QY 65 TRGLYEYANNSVGTIERYKKACSDAVNPPTITTEANTYYQOEASKLRQRDIQNLSNR 124

Db 65 SRGLYEYNSVSTIERYKKACSDSSNTGSVSEANAQYYQOEAAKLRSQIGNLSNR 124

QY 125 HILGESLGLNFKEKLNLESLEKGISRVSRKKHEMLVAEIEYMKREIEIQNDNMVLS 184

Db 125 NMLGESLSALSVKELKLEKIGIRSKKNELLFAEIEYMKREIDLHNNQLLRA 184

QY 185 KITERTGLOQESSVIHOGTVYESGVTSSHSGOYNRYIAVNLLPEPNQSSNQD 240

Db 185 KIAENE-RKRQHMNMLPGGVNFEIMQSPFDS----RNYSQVNGLPANHYPHEDQ 235

RESULT 10

AAB68438

ID AAB68438 standard; Protein; 238 AA.

XX AC AAB68438;

XX DT 23-JUL-2001 (first entry)

XX DE Amino acid sequence of the floral homeotic protein PTAG-2.

XX KW Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;

XX KW LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;

XX KW fertility; sterility.

XX OS Populus balsamifera.

XX


```
FH Key Location/Qualifiers
FT Domain 16..72
FT /note= "MADS domain"
FT Domain 106..172
FT /note= "K-domain"
XX
XX CA2319853-Al.
PN
XX
XX 01-APR-2001.
XX
XX 02-OCT-2000; 2000CA-2319853.
XX
XX 01-OCT-1999; 99US-0410464.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
XX
XX WPI; 2001-336098/36.
XX
XX N-PSDB; AAF85400, AAF85401, AAF85402.
XX
XX Novel isolated polynucleotide derived from Populus species, useful for
XX producing transgenic plants having modified fertility characteristic,
XX particularly sterility -
XX
XX Claim 23; Page 62-63; 69pp; English.
XX
XX The present sequence represents a floral homeotic protein, designated
XX PTAG-2, which is derived from Populus balsamifera subsp. trichocarpa.
XX The specification also describes PTD, PTLF, and PTAG-1 proteins. The
XX floral homeotic proteins are expressed in floral tissues. PTLF is a
XX homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in
XX immature inflorescences on which floral primordia are developing. PTD
XX is a homologue of DEFICIENS (DEF), and is strongly expressed in stamen
XX primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
XX homologues of AGAMOUS (AG). The floral homeotic proteins and
XX polynucleotides are useful for producing transgenic plants having
XX modified fertility characteristics, particularly sterility.
XX
XX Sequence 238 AA;
XX
XX Query Match 57.9%; Score 719.5; DB 22; Length 238;
XX Best Local Similarity 62.3%; Pred. No. 3.le-62;
XX Matches 147; Conservative 39; Mismatches 43; Indels 7; Gaps 3;
XX
XX 7 NEVAESS--KKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
XX || ||| :|||:|||||:| :|||:|||||:|||||:|||||:|||||:|
XX 5 NEPOESSPLRLGRGKVEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
XX :|||||:|||||:|||||:| :|||:|||||:|||||:|||||:|||||:|
XX 65 TRGRLEYANNVSRGTIERYKACSDAVNPPTITEANTQYQOQEAASKLRRIQDNLNR 124
XX :|||||:|||||:|||||:| :|||:|||||:|||||:|||||:|||||:|
XX 65 SRGRLEYSNNSVKSTIERYKACADSSNNGSVSEANAQFYQOQEAASKLRISQIGNLQNSNR 124
XX :|||||:| :|||||:|||||:| :|||:|||||:|||||:|||||:|||||:|
XX 125 HILGESLGNLKFELKLEKIGISRVRSKKHEMLVAEIEYMKREIELONDNMYLRS 184
XX :|||||:| :|||||:|||||:| :|||:|||||:|||||:|||||:|||||:|
XX 125 NMLGESLSALSVELKLEKIGIRSKKNEELFAEIEYMKREIDLHNNQLLRA 184
XX
XX 185 KITERTGLQQQESSVHOGTVESGTVSSHQSQGVNRYIAVNLLEPNQNSNQDQ 240
XX || | :|| :|| :| :| :| ||| || | :| :|
XX 185 KIAENE-RKRQHMLMPGVNFQINSQPFDS---RNYSQVNGLPANHYPHEDQ 235
XX
XX RESULT 11
XX ABG30868
XX ID ABG30868 standard; Protein; 238 AA.
XX
XX AC ABG30868;
XX
XX XX
XX 07-OCT-2002 (first entry)
XX
XX Poplar floral homeotic protein PTAG-2.
XX
XX Poplar; plant; DEFICIENS; transgenic; promoter;
XX
```

```
KW protein transduction domain; floral homeotic gene;
KW floral-specific expression; cytotoxin; fertility; sterility;
KW PTLF; PTAG-1; PTAG-2.
XX
XX OS Populus balsamifera subsp. trichocarpa.
XX
XX FH Location/Qualifiers
XX FT 16..72
XX FT /label= MADS_domain
XX FT /note= "MADS is named for the first 4 proteins in
XX FT which it was discovered, yeast minichromosome maintenance
XX FT factor, floral homeotic genes AG and DEF and human serum
XX FT response factor"
XX FT Domain 106..172
XX FT /label= K_domain
XX
XX US6395892-B1.
XX
XX 28-MAY-2002.
XX
XX 01-OCT-1999; 99US-0410464.
XX
XX 06-APR-1998; 98US-080851P.
XX
XX 06-APR-1999; 99US-0287700.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Strauss SH, Rottmann W, Brunner A, Sheppard L;
XX
XX WPI; 2002-572853/61.
XX
XX N-PSDB; ABK88490, ABK88491.
XX
XX New protein transduction domain promoter nucleic acid molecule useful
XX for producing transgenic plants having modified fertility
XX characteristics, particularly sterility -
XX
XX Disclosure; Column 81-84; 46pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule especially a
XX protein transduction domain (PTD) promoter: (i) that hybridises under
XX wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 %SDS (sodium
XX dodecyl sulphate) at 65 plusoc to nucleotides or (ii) comprising 35
XX consecutive nucleotides of the PTD gene. PTD is a floral homeotic
XX gene and is the homologue of DEFICIENS. Also includes are a recombinant
XX nucleic acid comprising the PTD promoter, a cell transformed with
XX the recombinant nucleic acid and a transgenic plant comprising the
XX transformed cell. The PTD promoter is useful to obtain floral-specific
XX expression of genes such as cytotoxins, that are employed in genetic
XX ablation strategies to produce trees having modified fertility
XX characteristics, including sterility. Genetic constructs comprising
XX antisense versions or dominant negative mutants of PTD are useful in
XX producing genetically engineered Poplars and other trees, and for sense
XX suppression. Also disclosed are 3 other homeotic genes PTLF, PTAG-1
XX and PTAG-2 (none are defined). The present sequence is the PTAG-2
XX protein.
XX
XX Sequence 238 AA;
```

```
Query Match 57.9%; Score 719.5; DB 23; Length 238;
Best Local Similarity 62.3%; Pred. No. 3.le-62;
Matches 147; Conservative 39; Mismatches 43; Indels 7; Gaps 3;
Qy 7 NEVAESS--KKIGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
Db || ||| :|||:|||||:| :|||:|||||:|||||:|||||:|||||:|
Qy 5 NEPOESSPLRLGRGKVEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
Db :|||||:|||||:|||||:| :|||:|||||:|||||:|||||:|||||:|
Qy 65 TRGRLEYANNVSRGTIERYKACSDAVNPPTITEANTQYQOQEAASKLRRIQDNLNR 124
Db :|||||:|||||:|||||:| :|||:|||||:|||||:|||||:|||||:|
Qy 65 SRGRLEYSNNSVKSTIERYKACADSSNNGSVSEANAQFYQOQEAASKLRISQIGNLQNSNR 124
Db :|||||:| :|||||:|||||:| :|||:|||||:|||||:|||||:|||||:|
Qy 125 HILGESLGNLKFELKLEKIGISRVRSKKHEMLVAEIEYMKREIELONDNMYLRS 184
Db :|||||:| :|||||:|||||:| :|||:|||||:|||||:|||||:|||||:|
Qy 125 NMLGESLSALSVELKLEKIGIRSKKNEELFAEIEYMKREIDLHNNQLLRA 184
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PR 06-JUL-1999; 99US-0142390.
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PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 28-JUL-1999; 99US-0145951.
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PR 26-AUG-1999; 99US-0150884.
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PR 25-OCT-1999; 99US-0161406.
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Search completed: January 27, 2003, 12:44:16
Job time : 31.3725 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:43:08 : Search time 13.4453 Seconds
(without alignments)
538.330 Million cell updates/sec

Title: US-09-978-382A-6

Perfect score: 1242

Sequence: 1 MEGGASNEVAESSKKIGRKK.....NLLEPNQSSNQDPPLQLV 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	714.5	57.5	252	1	US-08-460-512-5
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11	710.5	57.2	252	1	US-08-460-512-4
12	428.5	34.5	250	2	US-08-867-087B-13
13	421	33.9	273	2	US-08-592-214A-8
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16	421	33.9	273	3	US-08-655-241-8
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45	378	30.4	242	4	US-09-349-677-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-067-800-8
; Sequence 8, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-067-800-8

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; Sequence 8, Application US/09349677
; Patent No. 6286305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-349-677-8
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; Patent No. 6196024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-067-800-6
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; Sequence 6, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-349-677-6

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Db 241 DQPLQLV 248

RESULT 5
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; Sequence 7, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; APPLICATION NUMBER: US/08/293,278
; FILING DATE:
; APPLICATION NUMBER: US/07/956,694
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-512-7

Query Match 62.8%; Score 780.5; DB 1; Length 248;
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Qy 14 KIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGLVEYA 73
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Db 15 RKLGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGLVEYA 74
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Qy 74 NNSVRGTIERYKKACSDAVNPPTITEANTQYQOEAASKLRQIRDIQNLNHLIGESLGS 133
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Db 75 NNSVRGTIERYKKACSDSNTGTSISANAQYQOEAASKLRQIRDIQNLNHLIGESLAA 134
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Qy 134 LNFKELKNLESRLKGISRVRSKKHMLVAEIEYMQKRETELQNDNMVLRSKI--TERTG 191
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Db 135 LSLRDLKLEQIEKIGISKIRSKNELLFALIEYMQKREIDLHNNQYLRKIAETARAQ 194
| | | | |
Qy 192 LQQQSSV--IHOGTVYESGVTSQSQYNNRYIAVNLLEPNQSSNQDQPLQLV 246
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Db 195 QQQQQQMLMPGSSSYELVPPPHQFD--TRNYLQVNGLTNNHYTRQDQPSLQLV 248
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RESULT 6
US-09-433-579-2
; Sequence 2, Application US/09433579
; Patent No. 644877
; GENERAL INFORMATION:

```

; APPLICANT: Rottmann, William H.
; TITLE OF INVENTION: LSAG Gene
; FILE REFERENCE: LSAG Gene
; CURRENT APPLICATION NUMBER: US/09/433,579
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Liquidambar styraciflua
US-09-433-579-2

Query Match      61.6%; Score 764.5; DB 4; Length 226;
Best Local Similarity 67.5%; Pred. No. 2.1e-69;
Matches 156; Conservative 30; Mismatches 40; Indels 5; Gaps 2;

QY 16 IGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYANN 75
DB 1 MGRGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYANN 60

QY 76 SVRTIERYKACSDAVNPPTITEANTOYQOEASKLRQIRDIQNLRHILGESLGLN 135
DB 1 SVRTIERYKACSDAVNPPTITEANTOYQOEASKLRQIRDIQNLRHILGESLGLN 120

QY 136 FKEKLNLESRLKLGISRVRSKHEMLVAEIEYMQKRETELQNDNMNLYRSKIERTGLQOQ 195
DB 121 PKEKLGLETKLEKLGISRVRSKHEMLVAEIEYMQKRETELQNDNMNLYRSKIERTGLQOQ 180

QY 196 ESSVIHQGTVEYSGVSSHQSGQYNNRYIAVNLLEPNQSSNQDQPPLQ 246
DB 181 -MNLMPGGSNVEVLPSQPFDS----RNEFQVNALQNHHSYRQDQOMALQ 226

RESULT 7
US-09-410-464-12
; Sequence 12, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-12

Query Match      60.1%; Score 746.5; DB 4; Length 241;
Best Local Similarity 63.2%; Pred. No. 1.5e-67;
Matches 153; Conservative 41; Mismatches 41; Indels 7; Gaps 3;

QY 7 NEVAESS--KKGKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
DB 5 NESLESSPLRKLGRGKVEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64

QY 65 TRGRLEYANNVSGRTIERYKACSDAVNPPTITEANTOYQOEASKLRQIRDIQNLR 124
DB 65 SRGRLEYANNVSGRTIERYKACSDAVNPPTITEANTOYQOEASKLRQIRDIQNLR 124

QY 125 HILGESLGLNFKELKLEKISRVRSKHEMLVAEIEYMQKRETELQNDNMNLYRS 184
DB 125 HMLGESLGLNFKELKLEKISRVRSKHEMLVAEIEYMQKRETELQNDNMNLYRS 184

QY 185 KITERGLQOQESSVIHQGTVEYSGVSSHQSGQYNNRYIAVNLLEPNQSSNQD 240
DB 185 KIAENE--RKRQHMNMLPGGVNFEIMQSQPFDS----RNYSQVNGLPANHYPHEDQ 235

RESULT 9
US-08-460-512-5
; Sequence 5, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFISKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; APPLICATION NUMBER: US/08/460.512
; FILING DATE: 800
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/293.278
; FILING DATE:
; APPLICATION NUMBER: US/07/956.694
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-512-4

Query Match 57.2%; Score 710.5; DB 1; Length 252;
Best Local Similarity 58.4%; Pred. No. 7.1e-64;
Matches 146; Conservative 39; Mismatches 54; Indels 11; Gaps 4;

Qy 3 GGASNEVAESKKIGRGKIEKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVI 62
Db 8 GESS-----PORKAGRGKIEKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVI 63

Qy 63 FSTRGLYEYANNVSRGTIERKKACSDAVNPPTITEANTQYQOEASKLRQIRDIONL 122
Db 64 FSSRGLYEYNNVSGKTIERYKKALSDNSNTGSAEINAAQYQQESAKLRQIIISQNS 123

Qy 123 NRHILGESLGNFKELKNLESLRKGISRVRSKKHEMLVAEIEYMQKEIEIQLDNMVL 182
Db 124 NRQLMGETIGSMSPKRLNLEGRLDNRVNRIRSKNELLFAEIDYMQKEIEIQLDNMVL 183

Qy 183 RSKITERTGLOQOESSVTHOGVYEGSVTSSHSGO--YNNRYIAVNLLEPN---QNSS 236
Db 184 RAKIAENE-RNNPSMLMPGGSNYEIQIMPPTQTPQFDSRNYFYVAALQPNHHYSSAG 242

Qy 237 NQDOPPLQLV 246
Db 243 REDQALQLV 252

RESULT 12
US-08-867-087B-13
; Sequence 13, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Cynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan, E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-867-087B-13

Query Match 34.5%; Score 428.5; DB 2; Length 250;
Best Local Similarity 40.4%; Pred. No. 2.1e-35;
Matches 95; Conservative 44; Mismatches 73; Indels 23; Gaps 4;

Qy 16 IGRGKIEKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGLYEYANN 75
Db 1 MGRGRVLEKRIENKINQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSKSRGLYFSGA 60

Qy 76 SVRGTIERYKKACSDAVNPPTITEANTQYQOEASKLRQIRDIONLNRHILGESLGSIN 135
Db 61 GITKTLERYOHCYNAQDSNNAL-SETQSWYHEMSKKAKEALQRTQRHLLEDGLGPLS 119

Qy 136 FKEKLNLESLRKGISRVRSKKHEMLVAEIEYMQKEIRELQNDNNYLSKI-----TERT 190
Db 120 VKELQLEKLECALSAQRQKTQLMQEVLELRKKEQLGEINPQLKHKLEVEGSTSY 179

Qy 191 GLOOQESSVTHOGVYEGSVTSSHSGOYNNRYIAVNLLEPNQSSNQDQPLQL 245
Db 180 RAMQOASWA--QGAUVENG-----AAYVQPPPHSAAMDSEPTLQI 217

RESULT 13
US-08-592-214A-8
; Sequence 8, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592.214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (619) 535-9001
;
; TELEFAX: (619) 535-8949
;
; INFORMATION FOR SEQ ID NO: 8:
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 273 amino acids
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; TYPE: amino acid
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; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
US-08-592-214A-8

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[illegible]

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US-08-659-188-8

Query Match 33.9%; Score 421; DB 3; Length 273;
Best Local Similarity 37.3%; Pred. No. 1.4e-34;

Qy	16	IGRKIEIKRIENTNTNRQVFTCKRRNGLLKKAYELSVLCDAEVALVFTSTGRGLYEYANN	75
Db	1	MGRKVQLKRIENKINRQVFTSKRRNGLLKKAHEISVLCDAEVALVFTSPKGLYEYAD	60
Qy	76	SVRGTI----ERYKKACSDAVNPPTITEANTQYQQEASKLRQIRDIQNLNHLGESL	133
Db	61	SRMDKILLERYERYSAEKALISAESSEGN---WCHERYKLLKAKIETIQCHKHMGEDL	117
Qy	132	GSLNFELKNLESLEKGISRVKRSKKHEMIVAETEYMQKREIELQNDNMYLRSKITER--	189
Db	118	ESLNPKELQLEQOLDSSLKHIRSCKSHLMAESTSELQKKERSLQOEENKALQKELABROK	177
Qy	190	---TGLQOQSSVTHOQTVEYSGVTSHQS-----GQYNRN	222
Db	178	AVASRQOQOQOQVOWDOQTHAQOQTSSSSSSFFMRQOQGLPPPHNCTCFPLTMGRGEE	237
Qy	223	YIAVNLLEPNQNSNQDQPLQL	245
Db	238	LAAAAAQQOQOPLPGOQPOLRI	260

RESULT 15

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US-08-655-227-8
; Sequence 8, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APETALAL Gene
; DATE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,227
; FILING DATE: 05-JUN-1996

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Query Match 33.9%; Score 421; DB 3; Length 273;
Best Local Similarity 37.3%; Pred. No. 1.4e-34;
Matches 98; Conservative 43; Mismatches 86; Indels

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QY      16 IGRGKIEIKRIENTNRQVTFCKRRNGLLKAYEELSVCDAEVALVFSTRGRLEYANN 75
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```
Db 1 MGRGVQLKRIENKINROVTESKRNGLLKKAHEISVLCDAEVAVIVFSPKGKLYEYATD 60
Qy 76 SVRGTI----ERYKKACSDAVNPPTITEANTQYQOEASKLRROIRDIQNLRHILGESL 131
Db 61 SRMDKILERYERYSYAEKALISAESEGN---WCHYEYKRLAKAKIETIQKCHKHLMGEDL 117
Qy 132 GSLNFKELKNLESRLCKGISRVRSKKEHMLVAEIEYMKREIELOQNDNMYLRSKITER-- 189
Db 118 ESLNPKELQQLLEQQLDSSLKHRSRKSLSHMAESISELOKKERSLOEENKALOKELAEOK 177
Qy 190 ---TGLQOQESSVIHQGTVYESGVTSSHQS-----GQYNRN 222
Db 178 AVASRQOQQOQQVQWDQOQTHAQAOQTSSSSSPMMRQDQOGLPPPHNICFPPLTMGDRGEE 237
Qy 223 YIAVNLLEPNQSSNQDOPPLQL 245
Db 238 LAAAAAQQOQPLPQQAQPOLRI 260
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Search completed: January 27, 2003, 12:46:50
Job time : 14.4453 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:42:28 ; Search time 25.8947 Seconds
(without alignments)
1957.448 Million cell updates/sec

Title: US-09-978-382a-6

Perfect score: 1242
Sequence: 1 MEGASNEVAESSKIGRGK.....NLLEPNQSSNQDPPLQLV 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mhc.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.vertebrate.*
14: sp.unclassified.*
15: sp.rvirus.*
16: sp.bacteriaph.*
17: sp.bacteriaph.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1002	80.7	249	Q9AXZ1	Q9axz1 brassica na
2	845	68.0	244	Q9XHM3	Q9xhm3 liquidambar
3	829	66.7	225	Q93XH4	Q93xh4 vitis vinif
4	806	64.9	249	Q9MBE2	Q9mb22 rosa rugosa
5	801	64.5	242	Q8VWZ3	Q8vwz3 malus domes
6	775	62.4	247	Q04900	Q04900 petunia int
7	771	62.1	247	Q08711	Q08711 petunia hyb
8	768	61.8	242	Q9LEP2	Q9lep2 betula verr
9	767	61.8	242	Q9ZTV9	Q9z2v9 corvulus verr
10	763	61.5	246	Q9ZS30	Q9zs30 gerbera hyb
11	763	61.4	246	Q9ZS29	Q9zs29 gerbera hyb
12	759	60.1	246	Q9XFM8	Q9xfrm8 antirrhinum
13	746.5	60.1	239	Q8RWV5	Q8rvw5 phalaenopsi
14	746.5	60.1	241	Q06511	Q06511 populus tri
15	742.5	59.8	239	Q041195	Q041195 antirrhinum
16	738.5	59.5	228	Q9ZPK9	Q9zpk9 hyacinthus

17	738.5	59.5	248	10	Q41352
18	735	59.2	244	10	Q8RVK1
19	724	58.3	245	10	Q8VWZ2
20	722	58.1	225	10	Q9SBK3
21	719.5	57.9	238	10	Q065112
22	718.5	57.9	248	10	Q9ZRH4
23	716.5	57.7	236	10	Q9ARE9
24	712.5	57.4	248	10	Q9MBE1
25	710	57.2	229	10	Q04959
26	709	57.1	237	10	Q9SBK1
27	709	57.1	262	10	Q04958
28	705.5	56.8	254	10	Q43422
29	702	56.5	249	10	Q9MBE0
30	701.5	56.5	250	10	Q9MBD9
31	700.5	56.4	236	10	Q40704
32	700.5	56.4	247	10	Q0AWJ2
33	699.5	56.3	254	10	Q9SBK2
34	695.5	56.0	253	10	Q42457
35	695	56.0	249	10	Q9SBT4
36	690	55.6	208	10	Q948V3
37	686	55.2	221	10	Q9LKK1
38	681	54.8	234	10	Q8RU44
39	674	54.3	215	10	Q93XE3
40	672.5	54.1	228	10	Q40882
41	656	52.8	259	10	Q24009
42	653.5	52.6	232	10	Q8RU43
43	652	52.5	225	10	Q43616
44	650.5	52.4	222	10	Q9ZTY6
45	649.5	52.3	222	10	Q9S719

ALIGNMENTS

RESULT 1

Q9AXZ1	PRELIMINARY;	PRT;	249 AA.
ID	Q9AXZ1		
AC	Q9AXZ1:		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DE	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	SHATTERPROOF1.		
GN	BNSHP1.		
OS	Brassica napus (Rape).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid II; Brassicales; Brassicaceae; Brassica.		
OX	NCBI_TaxID=3708;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV, BRIDGER.		
RA	Pylatuk J.D., Davis A.R., Bonham-Smith P.C.;		
RT	"Molecular cloning and characterization of a B. napus SHP1 gene.;"		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Pylatuk J.D., Davis A.R., Bonham-Smith P.C.;		
RT	"Isolation of the coding region of Bnshp by RT-PCR.;"		
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
CC	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		
CC	-!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.		
DR	EMBL; AF228865; AAK00646.1; -.		
DR	EMBL; AY036062; AAK62033.1; -.		
DR	HSSP; P11746; 1MNM.		
DR	InterPro; IPR002487; TF_Kbox.		
DR	InterPro; IPR002100; TF_MADSbox.		
DR	Pfam; PF01486; K-box; 1.		
DR	Pfam; PF00319; SRP-TF; 1.		
DR	PRINTS; PR00404; MADSDOMAIN.		
DR	SMART; SM00432; MADS; 1.		
DR	PROSITE; PS00350; MADS_BOX_1; 1.		
DR	PROSITE; PS00666; MADS_BOX_2; 1.		
KW	DNA-binding; Nuclear protein; Transcription regulation.		

SQ	SEQUENCE	249 AA; 28219 MW; BE78E063E1F5FB4E CRC64;	
	Query Match	80.7%; Score 1002; DB 10; Length 249;	
	Best Local Similarity	82.7%; Pred. No. 1.8e-62;	
	Matches	205; Conservative 17; Mismatches 22; Indels 4; Gaps 3;	
QY	2	EGGASNEVAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALV 61	
Db	3	EGGSSHD--AESKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALV 61	
QY	62	IFSTRGLYEYANNSVGTIERYKKACSDAVNPPTITEANTQYQOESKLRQIRDION 121	
Db	62	IFSTRGLYEYANNSVGTIERYKKACSDAVNPPTITEANTQYQOESKLRQIRDION 121	
QY	122	LNRHILGESLGNFKELKNLESLEKGISRVRSKKHEMLVAEIEYMQKRETELQDNMY 181	
Db	122	SNRHIVGESLGNFKELKNLEGRLEKGISRVRSKKSELLVAEIEYMQKRETELQDNMY 181	
QY	182	LRSKITE--RTGLQOQESSVIHOGTVYESGVTS--OSGOYNNYIAVNLLPEPNQSSNQ 238	
Db	182	LRAKTEQARLNPEQHGSGVIOGTAVYESGLSSHDQSOHYNNRNYIPVNLLEPNQOFSQ 241	
QY	239	DQPPLQLV 246	
Db	242	DQPPLQLV 249	
RESULT 2			
ID	O9XHM3	PRELIMINARY; PRT; 244 AA.	
AC	O9XHM3;		
DT	01-NOV-1999 (TReMBLrel. 12, Created)		
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)		
DT	01-MAR-2002 (TReMBLrel. 20, Last annotation update)		
DE	Agamous homolog (Fragment).		
GN	LAG.		
OS	Liquidambar styraciflua (Amberboom) (Sweetgum tree).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Saxifragales; Hamamelidaceae; Liquidambar.		
OX	NCBI_TaxID=4400;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Liu J., Huang Y., Ding B., Tauer C.G.;		
RT	"cDNA cloning and expression of a sweetgum gene that shows homology		
RT	with Arabidopsis AGAMOUS."		
RL	Plant Sci. 142:73-82(1999).		
CC	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		
CC	-!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.		
DR	EMBL; AF103903; AAD38119.1; -.		
DR	HSSP; P11746; 1MNN.		
DR	InterPro; IPR002487; TF_Kbox.		
DR	InterPro; IPR002100; TF_MADSbox.		
DR	Pfam; PF01486; K-box; 1.		
DR	Pfam; PF00319; SRP-TF; 1.		
DR	PRINTS; PR00404; MADSDOMAIN.		
DR	SMART; SM00432; MADS; 1.		
DR	PROSITE; PS00350; MADS_BOX_1; 1.		
DR	PROSITE; PS50066; MADS_BOX_2; 1.		
KW	DNA-binding; Nuclear protein; Transcription regulation.		
FT	NON-TER 1		
SQ	SEQUENCE 244 AA; 28205 MW; A7BF0F928D52EA8 CRC64;		
	Query Match	68.0%; Score 845; DB 10; Length 244;	
	Best Local Similarity	71.1%; Pred. No. 1.5e-51;	
	Matches	172; Conservative 30; Mismatches 32; Indels 8; Gaps 4;	
QY	6	SNEVAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVFST 65	
Db	10	SSEGSSQKKMGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVFSS 69	
QY	66	RGRLEYANNVSVGTIERYKKACSDAVNPPTITEANTQYQOESKLRQIRDIONLRH 125	

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DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MADS-box protein.
GN MASAKO D1.
OS Rosa rugosa (Rugosa rose).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
OX NCBI_TaxID=74645;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FLOWER;
RA Vosman B., Smulders M.J.M.;
RX PubMed=10808068;
RA Kithara K., Matsumoto S.;
RT "Rose MADS-box genes 'MASAKO C1 and D1' homologous to class C floral
RT identity genes.";
RL Plant Sci. 151:121-134(2000).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AB025643; BAA90743.1; -.
DR HSSP; P11746; 1MNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 249 AA; 28796 MW; 16F5AC7857C17803 CRC64;

Query Match 64.9%; Score 806; DB 10; Length 249;
Best Local Similarity 67.1%; Pred. No. 8e-49;
Matches 167; Conservative 29; Mismatches 37; Indels 16; Gaps 5;

QY 5 ASNEVAESSKKIGRKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIES 64
Db 10 ADPESSQKLGKRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIES 69
QY 65 TGRGLYEYANNSVRGTTIERYKKACSDAVNPPTITEANTQYYQOEASKLRRIQDIONLR 124
Db 70 TGRGLYEYANNSVRATIERYKKAC-DSSNTGVSFTNQQFYQOEASKLRRIQDIONLR 128
QY 125 HILGESLGSNFKELKNLEKISGRVSRKKHMLVAEIEYMQKREIELQNDNNMYLRS 184
Db 129 HILGEALSTLNVKELKNLEKISGRVSRKKHMLVAEIEYMQKREIELQNDNNMYLRS 188
QY 185 KITERTGLOQOESSVIHQGTIVYESCVTSSHQSG-----QYRNRYIAVNLLEPNQ--NSSN 237
Db 189 KIAENDRAQQQQANMM-----PGLTSAIDQSPMPPOSYDRKSLFLV-ILESNNHHYNRQG 240
QY 238 QDQPLQLV 246
Db 241 QNQTPLQLV 249

RESULT 5
Q8VWZ3 PRELIMINARY; PRT; 242 AA.
AC Q8VWZ3;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE C-type MADS box protein.
GN MADS14.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
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RP SEQUENCE FROM N.A.
RC TISSUE=VEGETATIVE GROWING POINT;
RA van der Linden C.G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=VEGETATIVE GROWING POINT;
RA Vosman B., Smulders M.J.M.;
RT "Isolation of apple B- and C-type MADS box genes from vegetative
RT tissue.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251117; CAG80857.1; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE; PS00666; MADS_BOX_2; 1.
SQ SEQUENCE 242 AA; 27976 MW; 600B2A3595A37649 CRC64;

Query Match 64.5%; Score 801; DB 10; Length 242;
Best Local Similarity 67.5%; Pred. No. 1.7e-48;
Matches 164; Conservative 30; Mismatches 43; Indels 6; Gaps 2;

QY 6 SNEVAESS--KKIGRKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIF 63
Db 4 ANQAPESQTKLGRGKIEIKRIENTTNQVTFCKRRNGLLKAYELSVLCDAEVALVIF 63
QY 64 STRGLYEYANNSVRGTTIERYKKACSDAVNPPTITEANTQYYQOEASKLRRIQDIONLN 123
Db 64 STRGLYEYANNSVRATIDRYKKACADSDTGGSVSEANTQFYQOEASKLRRIQDIONLN 123
QY 124 RHILGESLGSNFKELKNLEKISGRVSRKKHMLVAEIEYMQKREIELQNDNNMYLR 183
Db 124 RHILGESLSTLNVKELKNLEKISGRVSRKKHMLVAEIEYMQKREIELQNDNNMYLR 183
QY 184 SKIERTGLOQOESSVIHQGTIVYESCVTSSHQSGQYRNRYIAVNLLEPNQSSNQDQPL 243
Db 184 AKIAESREQQQQTHMPGTSYD---PSMPNSYDRNFPFVILESNHHYPRQGOTAL 239
QY 244 QLV 246
Db 240 QLV 242

RESULT 6
Q40900 PRELIMINARY; PRT; 247 AA.
AC Q40900;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Agamous protein.
GN PAGL1.
OS Petunia integrifolia (Violet-flowered petunia) (Petunia inflata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PISTIL;
RA Karunanandaa B., Kao T.-h.;
RT "Characterization of a flower-specific cDNA of Petunia inflata
RT encoding a putative homolog of Agamous protein.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; L33973; AAA68001.1; -.
DR HSSP; P11746; 1MNM.
DR TRANSFAC; T03126; -.
RN [1]
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DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00350; MADS_BOX_2; 1.
DR PROSITE; PS00350; MADS_BOX_3; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 247 AA; 2839 MW; C1A5F1F0B6E9BECF CRC64;

Query Match 62.4%; Score 775; DB 10; Length 247;
Best Local Similarity 66.1%; Pred. No. 1.1e-46;
Matches 158; Conservative 31; Mismatches 50; Indels 0; Gaps 0;

QY 8 EVAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRG 67
DB 9 ESSSSQKSGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRG 68
QY 68 RLYEYANNSVRGTIERKKACSDAVNPPTITEANTQYQOEASKLRQIRDIQNLNRHIL 127
DB 69 RLYEYANNSVRATIDRYKKHHDSTSTGVSSEANTQYQOEAAKLRRQIRDIQTNRQIV 128
QY 128 GESLGSNFKELKNLESRLKESISVRSKKHEMLVAEIEYMKREIELONDNMVLSRKIT 187
DB 129 GEALSSLPDLKNLEKLEKKAIGRVRSKKNELLFSEIELMOKREIEMQNANMYLRAKIA 188
QY 188 ERTGLQQQESSVIHQGVYESSGVTSSSHOSGYNNRYIAVNLLPEPNQSSNQDPPQLQV 246
DB 189 EVERATQOMNLMFGGSEYQQQPMSSSTQPYDARNFLPVNLLPEPNPHYSRQDQTALQV 247

RESULT 7
Q08711 PRELIMINARY; PRT; 247 AA.
AC Q08711;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Fbp6 protein.
GN FBP6.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-W115; TISSUE=CARPEL;
RA Luw J.B.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-W115; TISSUE=CARPEL;
RA MEDLINE=94035167; PubMed=8106081;
RA Angenent G.C., Franken J., Busscher M., Colombo L., van Tunen A.J.;
RT "Petal and stamen formation in petunia is regulated by the homeotic
RT gene fbp1."
RL Plant J. 4:101-112(1993).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; X68675; CAA48635.1; -.
DR HSSP; P11746; 1MNN.
DR TRANSFAC; T03094; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00350; MADS_BOX_2; 1.
DR PROSITE; PS00350; MADS_BOX_3; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
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SQ SEQUENCE 247 AA; 28371 MW; 31B7A8D425199DA2 CRC64;

Query Match 62.1%; Score 771; DB 10; Length 247;
Best Local Similarity 66.1%; Pred. No. 2.2e-46;
Matches 158; Conservative 30; Mismatches 51; Indels 0; Gaps 0;

QY 8 EVAESSKKIGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRG 67
DB 9 ESSSSQKSGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRG 68
QY 68 RLYEYANNSVRGTIERKKACSDAVNPPTITEANTQYQOEASKLRQIRDIQNLNRHIL 127
DB 69 RLYEYANNSVRATIDRYKKHHDSTSTGVSSEANTQYQOEAAKLRRQIRDIQTNRQIV 128
QY 128 GESLGSNFKELKNLESRLKESISVRSKKHEMLVAEIEYMKREIELONDNMVLSRKIT 187
DB 129 GEALSSLPDLKNLEKLEKKAIGRVRSKKNELLFSEIELMOKREIEMQNANMYLRAKIA 188
QY 188 ERTGLQQQESSVIHQGVYESSGVTSSSHOSGYNNRYIAVNLLPEPNQSSNQDPPQLQV 246
DB 189 EVERATQOMNLMFGGSEYQQQPMSSSTQPYDARNFLPVNLLPEPNPHYSRQDQTALQV 247

RESULT 8
Q09LEP2 PRELIMINARY; PRT; 242 AA.
AC Q09LEP2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MADS box protein.
GN MADS6.
OS Betula verrucosa (White birch) (Betula pendula).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid I; Fagales; Betulaceae; Betula.
OX NCBI_TaxID=3505;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FEMALE INFLORESCENCE;
RA Lemmetyinen J., Elo A., Porali I., Sopanen T.;
RT "The ectopic expression of birch genes, BpMADS1 and BpMADS6, causes
RT homeotic changes in the flowers of tobacco and Arabidopsis."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AJ252071; CAB95649.1; -.
DR HSSP; P11746; 1MNN.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00350; MADS_BOX_2; 1.
DR PROSITE; PS00350; MADS_BOX_3; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 242 AA; 27977 MW; CEl12695AEDC5ED6 CRC64;

Query Match 61.8%; Score 768; DB 10; Length 242;
Best Local Similarity 66.2%; Pred. No. 3.5e-46;
Matches 155; Conservative 33; Mismatches 40; Indels 6; Gaps 3;

QY 14 KKGKRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYEA 73
DB 14 RKLGRGKIEIKRIENTTNQVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLEYEA 73
QY 74 NN-SVRGTIERKKACSDAVNPPTITEANTQYQOEASKLRQIRDIQNLNRHILCESLG 132
DB 74 NNSSVKTTIERKKACSAESSNGSGSVSEANTQYQOEAAKLRCQIRSVQNSRHILGEALS 133
QY 133 SLNFKELKNLESRLKESISVRSKKHEMLVAEIEYMKREIELONDNMVLSRKITERTGL 192
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Db 134 ELMFKELKNLEKLGKIRSKKNELLFAEIEYMQKRAELHNNNOILRAKIAENE-R 192
QY 193 OQOESSVTHOGTVYEGSVTSSHQSGYNNRYIAVNLLEPNQNSNODQPPQLQV 246
Db 193 NOQNLMVMPGGNGYELMQSQSDS----RTYFOVDALQPNHHYPRQDQIPLQLV 242

RESULT 9
Q92TV9 PRELIMINARY; PRT; 242 AA.
AC Q92TV9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
GN MADS1.
OS Corylus avellana (European hazel).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC eurosids I; Fagales; Betulaceae; Corylus.
OX NCBI_TaxID=13451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99084765; PubMed=9869420;
RA Rigola D., Pe M.E., Fabrizio C., Me G., Sari-Gorla M.;
RT "CaMADS1, a MADS box gene expressed in the carpel of hazelnut.";
RL Plant Mol. Biol. 38:1147-1160(1998).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF027376; AAD03486.1; -.
DR HSSP; P11746; 1MNN.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 2.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 242 AA; 6023 MW; 6D74CD8654A1B719 CRC64;

Query Match 61.8%; Score 767; DB 10; Length 242;
Best Local Similarity 65.8%; Pred. No. 4.1e-46;
Matches 154; Conservative 34; Mismatches 40; Indels 6; Gaps 3;

QY 14 KKGKRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 73
Db 14 RKLGRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEIALVIFSSRGRLYEYA 73
QY 74 NNSVKGTIERYKKACSDAVNPPTITEANTQYQQEASKLRROIRDIQNLRHILGESLG 132
Db 74 NNSVKGTIERYKKACSDSGSVSEANTQYQQEAAKLRQIRSVQDSNRHMLGEALS 133
QY 133 SLNFKELKNLESRLKGISRVRSKHEMLVAEIEYMQKREIELQNDNMVLRSKITETGL 192
Db 134 ELMFKELKNLEKGINRIRSKKNELLAEIYMHKREVDLHNNQFLRAKIAENE-R 192
QY 193 OQOESSVTHOGTVYEGSVTSSHQSGYNNRYIAVNLLEPNQNSNODQPPQLQV 246
Db 193 NOQNLMVMPGGNGYELMQSQSDS----RNYFOVDALQPNHHYPRQDQMALQLV 242

RESULT 10
Q92S30 PRELIMINARY; PRT; 264 AA.
AC Q92S30;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MADS-box protein, GAGAL.
GN GAGAL.
OS Gerbera hybrida.
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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Mutisieae; Gerbera.
OX NCBI_TaxID=18101;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. TERRA REGINA;
MEDLINE=99168221; PubMed=10069067;
RA Yu D., Kotilainen M., Poellainen E., Mehto M., Elomaa P.,
RA Helariutta Y., Albert V.A., Teeri T.H.;
RT "Organ identity genes and modified patterns of flower development in
Gerbera hybrida (Asteraceae).";
RL Plant J. 17:51-62(1999).
DR EMBL; AJ009722; CAA08800.1; -.
DR HSSP; P11746; 1MNN.
DR TRANSFAC; T04587; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
SQ SEQUENCE 264 AA; 30413 MW; 9930224484335798 CRC64;

Query Match 61.5%; Score 763.5; DB 10; Length 264;
Best Local Similarity 64.6%; Pred. No. 7.9e-46;
Matches 153; Conservative 34; Mismatches 43; Indels 7; Gaps 3;

QY 14 KKGKRGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSTRGRLYEYA 73
Db 31 RKMGGKIEIKRIENTTNROVTFCKRRNGLLKAYELSVLCDAEVALVIFSSRGRLYEYA 90
QY 74 NNSVKGTIERYKKACSDAVNPPTITEANTQYQQEASKLRROIRDIQNLRHILGE 129
Db 91 NNSVKGTIERYKKACSDAVNPPTISGTVAEANTQYQQEAAKLRQIANLQNRQFYRNIMGE 150
QY 130 SLGSLNFKELKNLESRLKGISRVRSKHEMLVAEIEYMQKREIELQNDNMVLRSKITER 189
Db 151 SLGDMPPVKDLKNLEKLEKAIISRIRAKKNELLFAEIEYMQKRELEHNSNQFLRAKIVEN 210
QY 190 TGLQOQESSVTHOGTVYEGSVTSSHQSGYNNRYIAVNLLEPNQNSNODQPPQLQV 246
Db 211 ERAQHHMSLMPGSSDYE--LVTPHQPD-GRNYLQTNLDLPNNDYSCDQTPQLQV 264

RESULT 11
Q92S29 PRELIMINARY; PRT; 246 AA.
AC Q92S29;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MADS-box protein, GAGA2.
GN GAGA2.
OS Gerbera hybrida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Mutisieae; Gerbera.
OX NCBI_TaxID=18101;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. TERRA REGINA;
MEDLINE=99168221; PubMed=10069067;
RA Yu D., Kotilainen M., Poellainen E., Mehto M., Elomaa P.,
RA Helariutta Y., Albert V.A., Teeri T.H.;
RT "Organ identity genes and modified patterns of flower development in
Gerbera hybrida (Asteraceae).";
RL Plant J. 17:51-62(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AJ009723; CAA08801.1; -.
DR HSSP; P11746; 1MNN.
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DR TRANSFAC; T04590; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SMO0432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00666; MADS_BOX_2; 2.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 246 AA; 28199 MW; CE7571754725CFA2 CRC64;

Query Match 61.4%; Score 763; DB 10; Length 246;
Best Local Similarity 64.6%; Pred. No. 7.8e-46;
Matches 159; Conservative 34; Mismatches 43; Indels 10; Gaps 5;

QY 7 NEVAESS--KKIGRGKIEKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 NDSGEMSPQKLGKIGKIEKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64

QY 65 TRGRLEYANNVSRGTIERKKACSDAVNPPTITEANTOYQOEASKLRQIRDIONLN- 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 SGRLEYANNVSRGTIERKKACSDAVNPPTITEANTOYQOEASKLRQIRDIONLN- 124

QY 124 ----RHILGESLGNFKELKNLESRLKIGISRVRSKKHEMLVAEIEYMQKRETELQNDNM 180
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 QFYRNMGESLGNMFKDLKNLESRLKIGIGKIRSKKNEILFAEIEYMQKRETELHNSNQ 184

QY 181 YLRSKITERTGLQOQESSVIHOGTVYESGVTSSHQSGQYNNRYIANVNLLEPNSSNQDQ 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 FLRSKIAENE-RAQQHMSLMPGSSDYE--LVAPHQFPD-GRNYLVQNDLPNNNSQDQ 240

QY 241 PPLQLV 246
   |||||
Db 241 TPLQLV 246

RESULT 12
Q9XFM8 PRELIMINARY; PRT; 246 AA.
AC Q9XFM8;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Farinelli protein.
GN FAR.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99353474; PubMed=10406807;
RA Davies B., Motte P., Keck E., Saedler H., Sommer H.,
RA Schwarz-Sommer Z.;
RT "PLENA and FARINELLI: redundancy and regulatory interactions between
RT two antirrhinum MADS-box factors controlling flower development.";
RL EMO J. 18:4023-4034(1999).
DR EMBL; AJ239057; CAB42988.1; -.
DR HSSP; P11746; IMNM.
DR TRANSFAC; T03208; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SMO0432; MADS; 1.
DR PROSITE; PS00666; MADS_BOX_2; 2.
SQ SEQUENCE 246 AA; 28144 MW; 91FF9813528F0813 CRC64;

Query Match 61.1%; Score 759; DB 10; Length 246;
Best Local Similarity 65.4%; Pred. No. 1.5e-45;
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Matches 159; Conservative 38; Mismatches 40; Indels 6; Gaps 4;

QY 6 SNEVAESSKKIGRGKIEKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFST 65
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 STEVS-PERKIGRGKIEKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSS 66

QY 66 RGRLEYANNVSRGTIERKKACSDAVNPPTITEANTOYQOEASKLRQIRDIONLNRH 125
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 RGRLEYANNVSRGTIERKKACSDAVNPPTITEANTOYQOEASKLRQIRDIONLN 126

QY 126 ILGESLGNFKELKNLESRLKIGISRVRSKKHEMLVAEIEYMQKR-EIQLONDNMWYLS 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 MLGESLGNFKELKNLESRLKIGISRVRSKKHEMLVAEIEYMQKRQEIQLHNNQYLSRA 186

QY 185 KITERTGLQOQESSVIHOGTVYESGVTSSHQSGQYNNRYIANVNLLEPNSSNQDQPL 243
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 KIAESRVQGHMMDPGGS---SGYEOLVETPPDARNYLOVNGLPQNDIPRODQLPL 243

QY 244 QLV 246
   |||
Db 244 QLV 246

RESULT 13
Q8RWV5 PRELIMINARY; PRT; 239 AA.
AC Q8RWV5;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE MADS-box transcription factor.
GN MADS1.
OS Phalaenopsis equestris.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Vandeeae; Aeridinae;
OC Phalaenopsis.
OX NCBI_TaxID=78828;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FLOWER BUD;
RA Chen H.H., Liu C.C., Tsuel S.W., Chen W.H.;
RT "Phalaenopsis equestris MADS-box protein (MADS1).";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF234617; AAL76415.1; -.
DR EMBL; AF234617; AAL76415.1; -.
SQ SEQUENCE 239 AA; 27731 MW; 6B96DB74B6592A5C CRC64;

Query Match 60.1%; Score 746.5; DB 10; Length 239;
Best Local Similarity 63.6%; Pred. No. 1.1e-44;
Matches 150; Conservative 41; Mismatches 40; Indels 5; Gaps 2;

QY 11 ESSKKIGRGKIEKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLY 70
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 EPKEMGRGKIEKRIENTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTRGRLY 66

QY 71 EYANVSRGTIERKKACSDAVNPPTITEANTOYQOEASKLRQIRDIONLNRRHILGES 130
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 EYANVSRGTIERKKACSDAVNPPTITEANTOYQOEASKLRQIRDIONLNRRHILGES 126

QY 131 LGSUNFKELKNLESRLKIGISRVRSKKHEMLVAEIEYMQKRQEIQLONDNMWYLSKITERT 190
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 LTTMSLRDLKOLETRLEKGIKIRAKKNELHAEIDYMQKREMELOTDMNFMRLNKISDNE 186

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ID O65111
AC O65111;
DT 01-AUG-1998 (Tremblrel. 07, Created)
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RT orientations of a transposon at the plena locus of Antirrhinum.";
RL Cell 72:85-95(1993).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; S53900; AAB25101.1; -.
DR HSSP; P11746; IMNM.
DR TRANSFAC; T03130; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00056; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 239 AA; 27662 MW; D48C6C18043F9682 CRC64;

Query Match 59.8%; Score 742.5; DB 10; Length 239;
Best Local Similarity 63.1%; Pred. No. 2e-44;
Matches 152; Conservative 38; Mismatches 44; Indels 7; Gaps 3;

QY 7 NEVAESSKKTGCKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFSTR 66
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QY 67 GRLYEYANNVSRGTIERYKACSDAVNPPTITEANTQYQAEASKLRRIQIRIOTSNRHI 126
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QY 127 LGESLGLSNFKELKNLESRLKGISRVRSKKHEMLVAEIEYQMKREIEIENDNMVLSKI 186
Db 125 LGEVSNMALKDLKSTEAQVKAISRSKKNELLFAETEHQMKRELEHNNMFLRAKI 184

QY 187 TERTGLQOQESSVTHOGTVYESGYTSSHQSGOYNRYTAVNLLPNQNS-SNODQPLQL 245
Db 185 AEGERAQOQMN--LMPGSDYQPMTSQSYDV----RNFLPMNLMPEPNQOQYSRHDQALQL 238

QY 246 V 246
Db 239 V 239

Search completed: January 27, 2003, 12:45:40
Job time : 26.8947 secs

DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
GN Agamous homolog.
GN PTAG1.
OS Populus trichocarpa (Western balsam poplar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Salicaceae; Populus.
OX NCBI_TaxID=3694;
RN [1]
RP SEQUENCE FROM N.A.
RA Brunner A.M., Rottmann W.H., Sheppard L.A., Strauss S.H.;
RT "Two Populus trichocarpa genes homologous to AGAMOUS.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF052570; AAC06237.1; -.
DR HSSP; P11746; IMNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00056; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 241 AA; 27559 MW; 4C2BFD1F29E99CF CRC64;

Query Match 60.1%; Score 746.5; DB 10; Length 241;
Best Local Similarity 63.2%; Pred. No. 1.1e-44;
Matches 153; Conservative 41; Mismatches 41; Indels 7; Gaps 3;

QY 7 NEVAESS--KKTGCKIEIKRIENTTNROVTFCKRRNGLLKKAYELSVLCDAEVALVIFS 64
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QY 245 LV 246
Db 240 LV 241

RESULT 15
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AC Q41195;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Ple protein.
GN PLE.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93137332; PubMed=8093684;
RA Bradley D., Carpenter R., Sommer H., Hartley N., Coen E.;
RT "Complementary floral homeotic phenotypes result from opposite

GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 06:06:04 ; Search time 42.9887 Seconds
(without alignments)
6391.971 Million cell updates/sec

Title: US-09-978-382A-3

Perfect score: 896

Sequence: 1 ggatcaatggaggaggtgg.....actgtgttttttcttca 896

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents.NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	344.8	38.5	1125	1	US-08-460-512-6
6	335.8	37.5	5622	4	US-09-067-800-3
7	335.8	37.5	5622	4	US-09-349-677-3
8	312.6	34.9	714	4	US-09-410-464-15
9	312.6	34.9	1159	4	US-09-410-464-14
10	305.2	34.1	723	4	US-09-410-464-11
11	305.2	34.1	1219	4	US-09-410-464-10
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13	284.4	31.7	1097	1	US-08-460-512-3
14	275.8	30.8	1457	1	US-08-460-512-1
15	188	21.0	6138	4	US-09-067-800-4
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17	159	17.7	498	4	US-09-073-587-6
18	149.2	16.7	1062	4	US-09-067-800-1
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22	143.2	16.0	1345	3	US-08-659-188-7
23	143.2	16.0	1345	3	US-08-655-227-7
24	143.2	16.0	1345	3	US-08-655-241-7
25	143.2	16.0	1345	3	US-09-149-976-7
26	143.2	16.0	1345	4	US-09-398-326-7
27	142.2	15.9	1043	2	US-08-867-087B-12

28	136	15.2	945	2	US-08-485-981-9	Sequence 9, Appli
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30	133.4	14.9	1141	2	US-08-323-449B-1	Sequence 1, Appli
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33	131.2	14.6	1180	2	US-08-867-087B-16	Sequence 16, Appli
34	128.6	14.4	794	1	US-08-592-214A-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
US-09-067-800-5
; Sequence 5, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 896 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..753
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 896
; OTHER INFORMATION: /note= "there is a poly(A) tail at
; OTHER INFORMATION: the end of the cDNA sequence."
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: 1..896
; OTHER INFORMATION: /note= "AGL1 cDNA and deduced
; OTHER INFORMATION: protein sequences."
; US-09-067-800-5

Query Match 100.0%; Score 896; DB 4; Length 896;
Best Local Similarity 100.0%; Pred. No. 5.2e-266; Indels 0; Gaps 0;
Matches 896; Conservative 0; Mismatches 0;

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RESULT 2
US-09-349-677-5
Sequence 5, Application US/09349677

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; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 896 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..753
; NAME/KEY: misc_feature
; LOCATION: 896
; OTHER INFORMATION: /note= "There is a poly(A) tail at
; OTHER INFORMATION: the end of the cDNA sequence."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..896
; OTHER INFORMATION: /note= "AGL1 cDNA and deduced
; OTHER INFORMATION: protein sequences."
; US-09-349-677-5
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Query Match 100.0%; Score 896; DB 4; Length 896;
Best Local Similarity 100.0%; Pred. No. 5.2e-266; Indels 0; Gaps 0;
Matches 896; Conservative 0; Mismatches 0;

QY 1 GGATCAATGGAGGAGGTGGGAGTAGTCACCGCAGAGAGTAGCAAGAAACTAGGGAGA 60
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RESULT 3

US-09-067-800-7
; Sequence 7, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 959 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 78..818
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..959
; OTHER INFORMATION: /note= "AGL5 cDNA and deduced
; OTHER INFORMATION: protein sequences."
US-09-067-800-7

Query Match 59.9%; Score 536.8; DB 4; Length 959;
Best Local Similarity 82.1%; Pred. No. 1.7e-155;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

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Qy 126 CAATGGTCTTCAAGAAAGCTTATGAACCTCTGCTGTGTGATGCGGAAGTTGCCCT 185
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Db 377 TAATACTCAGTACTATCAGCAAGAGGCGTCTAACTCCGAGAGACAGATTCGGGACATTCA 436
Qy 366 GAATTCAAATAGGCATATTGTTGGGAATCACTTGGTTCCTTGAACCTTCAAGGAACCTCAA 425
Db 437 GAATTTGAACAGACACATTTCTTGGTGAATCTCTTGGTTCCTTGAACCTTGAAGGAACCTCAA 496
Qy 426 AAACCTAGAGAGCGCTTTGAAAAGGAATCAGCCGTGTCGCTCCAAAAGAAATGAGCT 485
Db 497 GAACCTTGAAGTAGGCTTTGAGAAAGGAATCAGTCGTCGCTCCGATCCAAAGAGACGAGAT 556
Qy 486 GTTAGTGGCAGAGATAGATATATGAGAGAGGGAATGAGTTGCAACACAATAAAT 545
Db 557 GTTAGTTCAGAGATTGATATATGCAAAAAGGAATCGAGCTGCAAAAACGATAAAT 616
Qy 546 GTACCTGCGAGCAAGATAGCCGAAGGCCGAGATTGAATCCGGACCAAGAGGATTCGAG 605
Db 617 GTATCTCGCTCCAAGATTACTGAA-----AGAACAGGTCTACAGCAACAAGAAATCGAG 670
Qy 606 TGTGATACAAGGGACAGACAGTTTACCAATCCGGTGTATCTTCTCATGACCAAGTCCGAGCA 665
Db 671 TGTGATACATCAAGGGACAGTTTACAGTGGGGTGTACTTCTTCTCACCAGTCCGGGCA 730
Qy 666 TTATAATCGGAACCTATATTCCGGTGAACCTTCTTGAACCGCAATCAGCAATTCCTCCGGCCA 725

FILING DATE: 38.5%; Score 344.8; DB 1; Length 1125;
APPLICATION NUMBER: US/07/956,694
FILING DATE: 68.9%; Pred. No. 2.2e-96;
ATTORNEY/AGENT INFORMATION: Matches 488; Conservative 0; Mismatches 217; Indels 3; Gaps 1;
NAME: Irecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57322/RET
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 110..853
US-08-460-512-6

Query Match 38.5%; Score 344.8; DB 1; Length 1125;
Best Local Similarity 68.9%; Pred. No. 2.2e-96;
Matches 488; Conservative 0; Mismatches 217; Indels 3; Gaps 1;
QY 46 AAGAACTAGGAGAGGGGAAAAATAGATAAAGAGATAGAGACACAAACAAATCGTCAA 105
DB 152 AGGAACTGGAGAGGAGGAAATGAGATCAACGGATCGAAACACAAAGATCGTCAA 211
QY 106 GTTACTTTCGAAACGACGCAATGGTCTCTCAAGAAAGCTTATGAACCTCTCTGCTTG 165
DB 212 GTCACTTCTGCAAGAGCGCAATGGTTACTCAAAAGGCCATGAAATATCTGTGCTC 271
QY 166 TGTGATCGGAGTGGCCCTGCTGCTATCTCTCCACTCTGGCGCTCTCTATGATAGTCC 225
DB 272 TGTGATCTGAGTGTCTGTTGATGCTCTTCAAGCAGAGCGACACTCTATGATGATGC 331
QY 226 AACACAGTGTGAGGGGTACAAATGAAAGGTACAGAAAGCTTGTCCGATGCGTCAAC 285
DB 332 AACACAGTGTGAAAGCAACAATTCAGAGGTACAGAAAGCTTGTTCAGATTCCTCAAC 391
QY 286 CCTCTTCCTCCGTCAGGAGCTAATCTCAGTACTATCAGCAAGAACCTTAAGCTTCGG 345
DB 392 ACTGGTTCAATTTCCGAGGCCAATGCTCAGTATATCAGCAAGAACCTTCCAAATC 451
QY 346 AGGCAATTCAGATATTCAGAAATTCAGAAATAGCATATTTGGGGAATCACTGTTCC 405
DB 452 GCACAAATTCGAAATCTCAGAAATCAGAAACAGGACATGTTGGTGAATCACTGGTCA 511
QY 406 TTGAATTCAGAGGAATCAAAACCTAGAGGAGCTCTTTGAAAAGGAATCAGCCGCTGC 465
DB 512 CTGAGCCTCAGAGATCTGAGAAATCTGGAACAAAAATTTGAAAAGGCATACCAAAATC 571
QY 466 CGCTCCAAAAGATGAGCTGTAGTGCAGAGATAGATATATCGCAGAGAGGGAATG 525
DB 572 AGATCCAAAAGATGAGCTGCTGTTGCTGAAATTTGATATGATGATGAGAGGGAAT 631
QY 526 GAGTTCGAACAACAATACATGTACCTGCGGCAAGATAGCGGAGGCGCCAGCTGAAT 585
DB 632 GATTTCACAACAACAATCAGTACCTGAGAGCAAGATGCTGGAACCTGAGAGA---GCT 688
QY 586 CCGACAGCAGGAGGATCGAGTGTGATACAGGAGCAGACAGTTTACGAATCCGGTGTATCT 645
DB 689 CAGCAGCAGCAGCAGCAGCAGATGAATGATGCCAGGAGTTCAAGCTTATGAGCTT 748
QY 646 TCTCATGACCACTGCGAGCATTAATTCGGAACCTATATTCGGTGAACCTTCTTGAACCG 705
DB 749 GTCCCTCCACTCATCAATTTGATGATCTCGAAACCTATTACAAAGTTAATGGTTGCAACC 808
QY 706 AATCAGCAATTTCTCCGCCCAAGACCAACCTCTCTCAACTTGTGTAA 753
DB 809 AACACCAATTACACTACAGACAGCCACCACTCTCTTCAACTAGTCTAA 856

RESULT 6
US-09-067-800-3
Sequence 3, Application US/09067800
Patent No. 6198024
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Ferrandiz, Cristina
TITLE OF INVENTION: Seed Plants Characterized by Delayed
TITLE OF INVENTION: Seed Dispersal
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,800
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5622 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..5622
OTHER INFORMATION: /label= AG11_promoter
OTHER INFORMATION: /note= "Nucleotide sequence of the AG11 promoter."
US-09-067-800-3

Query Match 37.5%; Score 335.8; DB 4; Length 5622;
Best Local Similarity 99.4%; Pred. No. 2.8e-93;
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 558 AAAGATAGCCGAGGCGCAGATTGAATCCGAGCCAGCAGGAATCGAGTGATACAAGG 617
DB 5025 ATAGATAGCCGAGGCGCAGATTGAATCCGAGCCAGCAGGAATCGAGTGATACAAGG 5084
QY 618 GACGACAGTTTACGATCCGGTCTATCTCTCATGACCAGTCGCGAGCATTAATCGGAA 677
DB 5085 GACGACAGTTTACGATCCGGTCTATCTCTCATGACCAGTCGCGAGCATTAATCGGAA 5144
QY 678 CTATATCCGGTGAACCTTCTTGAACCGAATCAGCAATTCCTCCGCCAAGACCAACCTCC 737
DB 5145 CTATATCCGGTGAACCTTCTTGAACCGAATCAGCAATTCCTCCGCCAAGACCAACCTCC 5204
QY 738 TCTTCAACTGTGTAACTCAAAACATGATACTTGTTCCTCCCTCATACAGATTAAAG 797
DB 5205 TCTTCAACTGTGTAACTCAAAACATGATACTTGTTCCTCCCTCATACAGATTAAAG 5264
QY 798 GAGACGACGAGAGTTCATTTATATTTTATAACGCGACTGTGTATTCATAGTTAGGTT 857
DB 5265 GAGACGACGAGAGTTCATTTATATTTTATAACGCGACTGTGTATTCATAGTTAGGTT 5324
QY 858 TAATAATGATAATAACAAAACCTGTTGTTCTTTGCTTCA 896

Db	5325	TAATAATGATAATAACAARAACACTGTTGTTCTTTGCTTAA	5363
RESULT 7			
US-09-349-677-3			
; Sequence 3, Application US/09349677			
; Patent No. 6288305			
; GENERAL INFORMATION:			
; APPLICANT: Yanofsky, Martin F.			
; APPLICANT: Ferrandiz, Cristina			
; TITLE OF INVENTION: Seed Plants Characterized by Delayed			
; TITLE OF INVENTION: Seed Dispersal			
; NUMBER OF SEQUENCES: 24			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Campbell & Flores LLP			
; STREET: 4370 La Jolla Village Drive, Suite 700			
; CITY: San Diego			
; STATE: California			
; COUNTRY: United States			
; ZIP: 92122			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA: US/09/349,677			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 09/067,800			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Campbell, Cathryn A.			
; REGISTRATION NUMBER: 31,815			
; REFERENCE/DOCKET NUMBER: P-UD 2948			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (619) 535-9001			
; TELEFAX: (619) 535-8949			
; INFORMATION FOR SEQ ID NO: 3:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 5622 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: unknown			
; TOPOLOGY: unknown			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: 1..5622			
; OTHER INFORMATION: /label= AGLI_promoter			
; OTHER INFORMATION: /note= "Nucleotide sequence of the AGLI promoter."			
US-09-349-677-3			
Query Match 37.5%; Score 335.8; DB 4; Length 5622;			
Best Local Similarity 99.4%; Pred. No. 2.8e-93;			
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	558	AAAGATAGCCGAAGCGCCAGATTGAATCCGACAGCAGCAGGAATCGAGTGTGATACAAGG	617
Db	5025	ATAGATACCGAGCGCCAGATTGAATCCGACAGCAGGAATCGAGTGTGATACAAGG	5084
Qy	618	GACGACAGTTTACGAATCCGGTGTATCTCTCATGACCAGTGCAGCATTAATCGGAA	677
Db	5085	GACGACAGTTTACGAATCCGGTGTATCTCTCATGACCAGTGCAGCATTAATCGGAA	5144
Qy	678	CTATATTCGGTGAACCTCTTGAACCGAATCAGCAATCTCCGGCCAAAGACCAACTCC	737
Db	5145	CTATATTCGGTGAACCTCTTGAACCGAATCAGCAATCTCCGGCCAAAGACCAACTCC	5204
Qy	738	TCTTCAACTTGTGTAACCTCAAAACATGATAACTTGTTCCTCCCTCATAACGATTAA	797
Db	5205	TCTTCAACTTGTGTAACCTCAAAACATGATAACTTGTTCCTCCCTCATAACGATTAA	5264
US-09-410-464-15			
Query Match 34.9%; Score 312.6; DB 4; Length 714;			
Best Local Similarity 73.0%; Pred. No. 1.4e-86;			
Matches 402; Conservative 0; Mismatches 149; Indels 0; Gaps 0;			
Qy	46	AAGAACTAGGAGAGGAGGAATAAGAGATAGAGATAAGAGGATAGAGACACACAAATCGTCAA	105
Db	40	AGGAAGCTGGGAGGGGAAAGGTGGAGATCAAGCGATCGAGAACACCAACCAATCGCCAA	99
Qy	106	GTTACTTTCTGCAAAACGACCGAATGGTCTCTCAAGAAAGCTTATGAACTCTCTGCTCTT	165
Db	100	GTCACTTTCTGCAAAAGGCGGAATGGTTGCTCAAGAAAGCTTATGAAATTAATCTTCTT	159
Qy	166	TGTGATGCCGAAGTTGCCCTCGTCATCTCTCCACTCGTGGCCGCTCTATGAGTACGCC	225
Db	160	TGGATGCTGAGGTGGCACTCATCTCTTCCAGCCGTGGACGCTTTATGAGTACTCT	219
Qy	226	AACAACAGTGTGAGGGGTACAATTTGAAAGGTACAGAAAGCTTGTTCGATGCCGTCAAC	285
Db	220	AACAATAGTGTCAAAATCTACAATTTGAAAGGTACAAAAGGCAATGTGCAGATTTCTTCCAAC	279
Qy	286	CTCTCTTCCTCCAGCCGAGCTAATTAACACTAGTATCAGCAAGAGCCTTAAGCTTCGG	345
Db	280	AACGGGTGAGTTTCTGAAGCCAAATGCTCAGTCTATCAGCAAGAGCTGCGCAAGTGC	339
Qy	346	AGGAGATTCGAGATATTTCAGAAATTCAAATAGGCATATTGTTGGGGAATCACTTGGTTC	405
Db	340	TCGCAATTTGGTATTTCAGAAATTCAAACAGGAATATGCTGGGTGAATCACTTAGTGCA	399
Qy	406	TTGAACCTCAAGGAACCTCAAAACCTAGAGAGCGTCTTGAAGAGGAATCAGCCGTGTC	465
Db	400	TTGAGTGTGAGGAACCTTAAGAGCTTGGAGATAAAACCTTGAAAGAGGAATTCGTTAGAAT	459
Qy	466	CGCTCCAAAAGAAATGAGCTCTTAGTGGCAGAGATAGATATATCAGAAAGAGGAAATG	525
Db	460	CGTTCGAAAAGAAATGAGCTCTTGTTCGCTGAATTTAGTATATCAGAGAGGAGATT	519
Qy	526	GAGTTCGAACACAATAACATGATCTACCTCGAGCAAGAGATAGCGAAGGCCCGCATTTGAAT	585

Db 520 GACTTGCAACAATAACCAGCTTCTCCGAGCAAAAGATTGCAGAGATGAAGAAAGCGA 579
Qy 586 CCGGACCAGCA 596
| | | | |
Db 580 CAGCACATGAA 590
| | | | |
RESULT 9
US-09-410-464-14
; Sequence 14, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1159
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (99)...(815)
US-09-410-464-14
Query Match 34.9%; Score 312.6; DB 4; Length 1159;
Best Local Similarity 73.0%; Pred. No. 1.8e-86;
Matches 402; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
Qy 46 AAGAACTAGGAGAGGGGAAATAGAGATAAGAGGATAGAGAACACAAATCGTCAA 105
| | | | |
Db 138 AGGAGCTGGGAGGGGAAGGTGGAGATCAAGCGATCAGAGACACCAATCGGCAA 197
| | | | |
Qy 106 GTTACTTTCGAAACGACGCAATGTCTTCTCAAGAAAGCTTATGAACCTCTGTCTTG 165
| | | | |
Db 198 GTCACTTTCGAAAAGGGGAATGGTTTCTCAAGAAAGCCTATGAATATCTGTCTT 257
| | | | |
Qy 166 TGTGATGCGGAAGTTGCCCTCGTCATCTTCTCCACTCGTGGCGCTCTATGAGTAGGCC 225
| | | | |
Db 258 TCGGATGCTGAGGTGCATCTCATCTCTTCTCCAGCGCTGGACGCCCTTTATGAGTACTCT 317
| | | | |
Qy 226 AACACAGTGTGAGGGGTACAATTGAAAGGTACAAGAAAGCTTGTCCGATGCCGTCAAC 285
| | | | |
Db 318 AACAAATGTCAAACTACAATTGAAAGGTACAAGAAAGCATGTGCAGATTCTTCCAAC 377
| | | | |
Qy 286 CCTCCTTCGTCACCAAGCTAATFACTCAGTACTATCAGCAAGAGCCTCTAAGCTTCGG 345
| | | | |
Db 378 AACGGGTGAGTTCTTCAAGCAATGTCTCAGTCTTATCAGCAAGAGCTGCCAAGTCCGC 437
| | | | |
Qy 346 AGGCAGATTTCGAGATATTCAGAAATTCAAATPAGGCATATTGTGGGGAATCACTTGGTTCC 405
| | | | |
Db 438 TCGCAAAATGGTAATTGCGAATTCAAACAGGAATATGCTGGGTGAATCAGTTAGTCA 497
| | | | |
Qy 406 TTGAAGTTCAGAACTCAAAACCTTAGAGAGGAGTCTTCAAGAAAGAAATCAGCCGTGTC 465
| | | | |
Db 498 TTGAGTGTGAAGAACTTAGAGCTTGGAGATAAACTTGAAGAAAGAAATTTGTAAGATT 557
| | | | |
Qy 466 CGCTCCAAAAGAAATGAGCTGTTAGTGGCAGAGATAGAGTATATGCAAGAGAGGGAATG 525
| | | | |
Db 558 CGTTCGAAAAGAAATGAGCTGTTGTTGCTGAAATGAGTATATGCAAGAGAGGAGATT 617
| | | | |
Qy 526 GAGTTGCAACAATAAACATGTACCTTCGAGCAAAAGATAGCCGAGCGCCAGATTGAAT 585
| | | | |
Db 618 GACTTGCAACAATAACCAGCTTCTCCGAGCAAAAGATTGCAGAGATGAAGAAAGCGA 677
| | | | |

Qy 586 CCGGACCAGCA 596
| | | | |
Db 678 CAGCACATGAA 688
| | | | |
RESULT 10
US-09-410-464-11
; Sequence 11, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(723)
US-09-410-464-11
Query Match 34.1%; Score 305.2; DB 4; Length 723;
Best Local Similarity 73.2%; Pred. No. 2.7e-84;
Matches 391; Conservative 0; Mismatches 143; Indels 0; Gaps 0;
Qy 46 AAGAACTAGGAGAGGGGAAATAGAGATAAGAGGATAGAGAACACAAATCGTCAA 105
| | | | |
Db 40 AGGAACTGGGAAGGGGAAAGGTGGAGATCAAGCGATCAGAAACACCAATCGGCAA 99
| | | | |
Qy 106 GTTACTTTCGAAACGACGCAATGTCTTCTCAAGAAAGCTTATGAACCTCTGTCTTG 165
| | | | |
Db 100 GTCACTTTCGAAAAGGGCGAGTGGTTTGTCTCAAGAAAGCCTACGAATATCTGTCTT 159
| | | | |
Qy 166 TGTGATGCGGAAGTTGCCCTCGTCATCTTCTCCACTCGTGGCGCTCTATGAGTAGGCC 225
| | | | |
Db 160 TCGATGCTGAGTGTGCATCTCATCTCTCTAGCGCGCTGCCTTTATGAGTACTCT 219
| | | | |
Qy 226 AACACAGTGTGAGGGGTACAATTGAAAGGTACAAGAAAGCTTGTCCGATGCCGTCAAC 285
| | | | |
Db 220 AACGATAGTGTCAAAATCAACAATTGAGAGGTACAAAAGGCATCTGCAGATTCTTCAAC 279
| | | | |
Qy 286 CCTCCTTCGTCACCAAGCTAATFACTCAGTACTATCAGCAAGAGCCTCTAAGCTTCGG 345
| | | | |
Db 280 ACTGGGTGTTTCTGAAGCAATGTCTCAGTACTACCAAGCAAGAGTGCAGCTGGGT 339
| | | | |
Qy 346 AGGCAGATTTCGAGATATTCAGAAATTCAAATPAGGCATATTGTGGGGAATCACTTGGTTCC 405
| | | | |
Db 340 TCCCAAAATGGTAATTGCGAATTCAAACAGGCATATGCTGGGTGAAGCGCTTAGTTCA 399
| | | | |
Qy 406 TTGAAGTTCAGAACTCAAAACCTTAGAGAGGAGTCTTCAAGAAAGAAATCAGCCGTGTC 465
| | | | |
Db 400 TTGAGTGTGAAGAACTTAGAGTTTGGAAATACGACTTTCGAAAGGAATNAGCAGAAAT 459
| | | | |
Qy 466 CGCTCCAAAAGAAATGAGCTGTTAGTGGCAGAGATAGAGTATATGCAAGAGAGGGAATG 525
| | | | |
Db 460 CGTTCGAAAAGAAATGAGCTGTTGTTTGCAGAAATCAGTATATGCAAGAGAGGAGGTT 519
| | | | |
Qy 526 GAGTTGCAACAATAAACATGTACCTTCGAGCAAAAGATAGCCGAGCGCCAGCA 579
| | | | |
Db 520 GACTTGCAACAATAACCAGCTTCTCCGAGCAAAAGATTTCAGAGATGAAGAA 573
| | | | |
RESULT 11

US-09-410-464-10
; Sequence 10, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; TITLE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1219
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(921)
US-09-410-464-10

Query Match 34.1%; Score 305.2; DB 4; Length 1219;
Best Local Similarity 73.2%; Pred. No. 3.5e-84;
Matches 391; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 46 AAGAACTAGGAGAGGAGGAAATAGAGATAAAGAGATAGAGAACACACAAATCGTCAA 105
Db 235 AGGAGCTGGGAGGGAAGGTGAGATCAAGCGATCGAGAACACACCACCAATCGCCAA 294
Qy 106 GTTACTTTCTGCAACAGCAGCAATGGTCTTCTCAGAAAGCTTATCAACTCTCTGCTTG 165
Db 295 GTCACCTTTCTGCAAAAGCGCAGTGGTTGCTCAAGAAAGCGCTACGAATATCTGTTCTT 354
Qy 166 TGTGATGCCGAAGTTGCCCTCGTCTATCTTCTCAGTCTGTCGCGCTCTATGAGTACGCC 225
Db 355 TCGGATGTGAGTTGCACTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 414
Qy 226 AACACAGTGTGAGGGGTACAAATGAAAGGTACAGAAAGCTTTGTCGATGCCGTCAC 285
Db 415 AACGATGTGCAAAATCAAAATGAGAGGTACAGAAAGCGCTCTGCAATCTTCAAAAC 474
Qy 286 CCTCTCTCGTCACCGAGCTAATCTCAGTACTATCAGCAAGAGCGCTCTTAAGCTTCGG 345
Db 475 ACTGGTCTGTTCTGAAGCCATGCTCAGTACTCTCTCTCTCTCTCTCTCTCTCTCTCT 534
Qy 346 AGGCAGATTCGAGATATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTC 405
Db 535 TCCCAATTTGGTAATTTGAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTC 594
Qy 406 TTGAATCTCAAGAACTCAAAACCTAGAGAGCTCTTGAAGAAAGCTTCAAGAAAGCTT 465
Db 595 TTGAGTGTGAAGAACTTAAAGTGTGGAATACAGTCTTGAAGAAAGCTTCAAGAAAGCT 654
Qy 466 CCCTCCAAAGAAATGAGCTGTGTTGAGCAGAGATAGATATATGAGAAAGCTTCAAGAA 525
Db 655 CGTTCCTCAAGAAATGAGCTGTGTTGAGCAGAAATTCAGAAATTCAGAAATTCAGAA 714
Qy 526 GAGTGTCAACAAATCAATGATACCTCGGAGCAAGATAGCCGAGCGCCAGA 579
Db 715 GACTGTCAACAAATCAACAGCTTCTCCGAGCAAGATTTCAAGAAATGAGAA 768

RESULT 12
US-09-433-579-1
; Sequence 1, Application US/09433579
; Patent No. 6444877
; GENERAL INFORMATION:
; APPLICANT: Rottmann, William H.
; TITLE OF INVENTION: LSAG Gene

; FILE REFERENCE: LSAG Gene
; CURRENT APPLICATION NUMBER: US/09/433,579
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1297
; TYPE: DNA
; ORGANISM: Liquidambar styraciflua
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (331)..(1008)
US-09-433-579-1

Query Match 32.1%; Score 287.8; DB 4; Length 1297;
Best Local Similarity 65.5%; Pred. No. 8.2e-79;
Matches 462; Conservative 0; Mismatches 222; Indels 21; Gaps 2;

Qy 49 AAACACTAGGAGAGGAGGAAATAGAGATAAAGAGGATAGAGAACACACAAATCGTCAAGTT 108
Db 328 AAAATGGGTAGGGGAAAGATCGAGATCAAGCGGATCGAGAACACGACGACAAACCGCAAGTC 387
Qy 109 ACITTCTGCAACAGCAGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTTGTTGT 168
Db 388 ACCTTCTGTAACCGCGCAACGGCTTACTCAAGAGGCGCTATGAATTAATCTGTTCTCTGT 447
Qy 169 GATGCCGAAGTTGCCCTCGTCATCTTCTCCACTCGTGGCGCTCTCTATGAGTACGCCAAC 228
Db 448 GATGCCGAGGTAGCCCTTATCGTCTTCTTACCCTGTCGCGCTTACGAGTATGCCAAC 507
Qy 229 AACAGTGTGAGGGGTACAAATGAAAGGTACAAAGAAAGCTTTTCGGATGCGCTCAACCTT 288
Db 508 AACAGTGTAAAGCAACAATGAGAGGTATAGAGGCGATCTGTGATTCCTTCCCAATCT 567
Qy 289 CCTTCCCTCCAGGAGCTAATCTCAGTACTATCAGCAAGAGCGCTCTAAGCTTCGGAGG 348
Db 568 GGATCTCTTCTGAAGCAATGCTCAGTCTTACAGCAAGAGCTGCGCAACTGCGTAAC 627
Qy 349 CAGATTCAGATATTCAGAAATTCAGAAATGAGCATATGTTGGGGAATCACTTGGTTCCTTG 408
Db 628 CAATCAGGAATATGCAGAAATACAAACAGGACTATGCTGGGTGAGTCTTTGGGCTCTCTG 687
Qy 409 AACTTCAAGGNACTCAAAACCTAGAGGAGCTCTTGAAGAAAGGAAATCAGCGCTGTCCGC 468
Db 688 AGTCCCAAGAACTCAAGGAGCTTGGAGGCTTGGAGCTAATTAGAGAAAGGCTTAGCAAAATAGG 747
Qy 469 TCCAAAAGAAATGAGCTGTTAGTGGCAGAGATAGAGTATATGCAAGAGGAAATGGAG 528
Db 748 TCCAAAAGAAATGAGCTGTTTCCGAAATTAATACATGCAAAAGAGGAAATCGAC 807
Qy 529 TTGCAACACAATAACATGTACCTGGGAGCAAGATAGCGGAAGCGCCAGATTAATCCG 588
Db 808 TTGCACAATGATACCCAGTATCTCCGAGCAAAATAGCTGAACACGAGAGA ----- 858
Qy 589 GACCAGCAGGAAATCGAGTGTATCAAGGAGGAGCAGCTTTACGAATCCGGTGTATCTTCT 648
Db 859 GCTCAACAGCAAAATGAACTTGAAGCCAGTGGATCAAACTATGAGTCTTGGCATC --- 914
Qy 649 CATGACCAGTGCAGCAATTAATCGGAACCTATATTCGGGTGAACCTTCTTGAACGAAT 708
Db 915 -----ACAGCCATTTGACTCTCGGAACCTTTTCCAAAGTAAATGCAATGCAACCAAT 966
Qy 709 CAGCAATTTCTCGGCGCAACCAACCTCTCTTCAACTTGTGTAA 753
Db 967 CATCATTTACTCTCGCAAGATCAAAATGGCCCTTCAATTAGTTAA 1011

RESULT 13
US-08-460-512-3
; Sequence 3, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.

APPLICANT: YANOFKY, Martin F.
APPLICANT: MA, Hong
TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,512
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/293,278
FILING DATE:
APPLICATION NUMBER: US/07/956,694
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57322/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1097 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 126..884
US-08-460-512-3

Query Match 31.7%; Score 284.4; DB 1; Length 1097;
Best Local Similarity 70.3%; Pred. No. 8.4e-78;
Matches 381; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 46 AGAAGACTAGGAGAGGAGAAATAGAGATAAGAGGATAGAGACACACAAACATCGTCAA 105
DB 168 AGGAAAGCTGGGAGAGGAGAAATAGAGATAAGAGGATAGAGACACACAAACATCGTCAA 227
QY 106 GTTACTTTCTGCAACACGCAATGCTTCTCAAGAAAGCTTATGAACCTCTCTGCTTTG 165
DB 228 GTTACTTTCTGCAACACGCAATGCTTCTCAAGAAAGCTTATGAACCTCTCTGCTTTG 287
QY 166 TGTGATGCCGAAGTTGCCCTCGTCATCTTCTCCACTCGTGCCCGTCTCTATGAGTACGCC 225
DB 288 TGTGATGCTGAAGTCGCACTCATTTCTCTCTAGCCGTCGCGCTCTCTATGAGTACCA 347
QY 226 AACACAGCTGAGGGGTACAAATGAAGGTACAAAGAGCTTGTTCGATGCCGTCAAC 285
DB 348 AACACAGCTGAGGGGTACAAATGAAGGTACAAAGAGCTTGTTCGATGCCGTCAAC 407
QY 286 CTTCTCTCCGTCACCGAAGTAACTACTCAGTACTATCAGCAAGAGCCTCTAAGCTTCGG 345
DB 408 ACCGGATCCGTGGCAGAAATTAATGCACAGTATTATCAACAAGATCTGCCAAATTCGCT 467
QY 346 AGGAGATTCGAGATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTCAG 405
DB 468 CAACAAATATACGATACAGCACTCGAAGCAATTCAGAAATTCAGAAATTCAGAAATTCAG 527
QY 406 TTGAACCTTCAAGGAACCTCAAAACCTTAGAGAGACGCTCTTTGAAAGGAATCAGCCGTGTC 465

DB 528 ATGTCTCCCAAGAGCTCAGAACTTGGAAAGCAGATAGACAGAAAGTGTATATCGAATC 587
QY 466 CGCTCCAAAAGAAATGAGCTGTAGTGGCAGAGATAGATATATGAGAAAGAGGAAATG 525
DB 588 CGATCCAGAAGAACGAACTCTTATTCGCGGAANTGACTACATGCAAGAGAGAAATG 647
QY 526 GAGTTGCAACAAATAACATGACTACCTCGGCGCAAGAAAGATAGCCGAGGCGCAGATTGAAT 585
DB 648 GATTTGCATAACGATAACCAAGCTTCTCTGCTTAAGATAGCTGAAATGAGAGAAAT 707
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DB 708 CC 709
RESULT 14
US-08-460-512-1
Sequence 1, Application US/08460512
Patent No. 5744693
GENERAL INFORMATION:
APPLICANT: MEYEROWITZ, Elliot M.
APPLICANT: YANOFKY, Martin F.
APPLICANT: MA, Hong
TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,512
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/293,278
FILING DATE:
APPLICATION NUMBER: US/07/956,694
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57322/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1457 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 416..1270
US-08-460-512-1

Query Match 30.8%; Score 275.8; DB 1; Length 1457;
Best Local Similarity 69.2%; Pred. No. 4.3e-75;
Matches 376; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

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DB 557 AGGAATCTGGAGAGGAGAAATAGAGATAAGAGGATAGAGACACAAACATCGTCAA 616

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QY	166	TGT	GATGGCGGAAGTTGCCCTCGTCTATCTTCTCCACTCGTGGCCGCTCTCTATGATGAGTCGCC		225
Db	677	TGT	GATGCTGAAGTCGCACCTCATCGTTTCTCTAGCCGCTGGTCTCTATGAGTACTCT		736
QY	226	ACA	CACAGTGTGAGGGGTACAAATGAAAGGTACAAGAAAGCTTCCCGATGCGCTCAAC		285
Db	737	ACA	CACAGTGTAAAGGTACTATTGACAGGTTACAAGAGGCAATATCGACAAATCTTAAC		796
QY	286	CCT	CTCTTCGGTCACCGAAGCTTAATACTCAGTACTATCAGCAAGAAGCCTCTAAGCTTCGG		345
Db	797	ACG	GATCGGTGGCAGAAATTAATGCACAGTATTATCAACAAGAAATCAGCCAAATTCGCT		856
QY	346	AGC	CAGATTCGAGATATTTCAGAAATCAATAGAGCATATGTTGGGGAATCAGTTGGTTCC		405
Db	857	CAAC	AAATTTATCAGGATACAAACCTCCAACAGGCAATGATGGGTGAGACATAGAGGTCA		916
QY	406	TTG	AACCTCAAGGAACCTCAAAAACCTAGAAGGAGCTCTTGAAAAGGAATCAGCCGTGC		465
Db	917	ATG	CTCCCAAGAGCTCAGGNACTTGAAGCGAGATTAGAGACAAGTATTACC	GAAATC	976
QY	466	CGT	CTCAAAAAGATGAGCTGTTAGTGGCAGAGATAGAGTATATGCAGACAGGGAATG		525
Db	977	CGA	TCCAAGAAATGAGCTCTATTTTCTGAAATCGACTACATCGAGAAAAGAGAAAGTT		1036
QY	526	GAG	TTCACACAAATTAACATGTACCTCGCAGCAAGATAGCCGAAGCGCCACATTTGAAT		585
Db	1037	GAT	TTCATACGATATACCAGATCTTCGTGCATAGATAGCTGAAATGAGAGGAACAAT		1096
QY	586	CCG	CCG	588	
Db	1097	CCG	CCG	1099	

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 08:21:19 ; Search time 1623.91 Seconds
(without alignments)
8935.939 Million cell updates/sec

Title: US-09-978-382a-3

Perfect score: 896

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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8: em_htc:*
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27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	319.8	35.7	715	BI933168	BI933168 EST53057
2	315.4	35.2	686	BQ411600	BQ411600 GA_Ed004
3	313.8	35.0	656	BQ411583	BQ411583 GA_Ed004
4	312.4	34.9	748	BI311095	BI311095 EST531284
5	311.6	34.8	624	10 AW277843	AW277843 sf87d01.y
6	306.4	34.2	754	BI310910	BI310910 EST531266

7	302.4	33.8	636	14	BQ123247	BQ123247 EST608823
8	299.8	33.5	656	10	BE659918	BE659918 1299 Gmax
9	299	33.4	548	10	AW277299	AW277299 sf80e05.y
10	295.8	33.0	548	10	BE434089	BE434089 EST405167
11	292.2	32.6	555	13	BI272847	BI272847 NF097G09F
12	290.6	32.4	538	10	BE433121	BE433121 EST399650
13	288	32.1	776	12	BG445079	BG445079 GA_Ea002
14	288	32.1	866	12	BG441292	BG441292 GA_Ea001
15	288	32.1	892	12	BG444639	BG444639 GA_Ea002
16	286	31.9	597	9	AI729115	AI729115 BNIGH1126
17	285.8	31.9	642	9	AI725968	AI725968 BNIGH1137
18	281.4	31.4	802	13	BI925669	BI925669 EST545558
19	280.2	31.3	960	12	BG445265	BG445265 GA_Ea002
20	278.6	31.1	754	9	AI731375	AI731375 BNIGH1938
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22	276.4	30.8	632	10	AW185524	AW185524 se80h09.y
23	275.6	30.8	848	12	BG445047	BG445047 GA_Ea002
24	274	30.6	649	10	AW184799	AW184799 se82f12.y
25	273.4	30.5	929	12	BG444491	BG444491 GA_Ea002
26	272.8	30.4	562	9	AI727662	AI727662 BNIGH1854
27	271.8	30.3	607	10	AW705451	AW705451 sk9c05.y
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29	269.8	30.1	539	9	AI771796	AI771796 EST252896
30	267.2	29.8	811	17	AQ250561	AQ250561 T12C11-Sp
31	266.4	29.7	498	12	BF112843	BF112843 EST440433
32	265.2	29.6	537	9	AI486290	AI486290 EST244611
33	262.8	29.3	608	10	AW278878	AW278878 sf99h09.y
34	262	29.2	615	10	AV557878	AV557878 7-H4 Gmax
35	261	29.1	698	10	BE659915	BE659915 7-H4 Gmax
36	260.4	29.1	586	12	BG446848	BG446848 GA_Eb003
37	260	29.0	597	10	AW704750	AW704750 sk55a06.y
38	258.2	28.8	566	9	AI728519	AI728519 BNIGH1109
39	257.2	28.7	618	9	AI484747	AI484747 EST243008
40	255.2	28.5	754	13	BI311053	BI311053 EST531280
41	251.4	28.1	613	10	BE659913	BE659913 3-D9 Gmax
42	249.8	27.9	550	10	BE494811	BE494811 WHE1273.H
43	249.4	27.8	468	10	BE431937	BE431937 EST398466
44	245.8	27.4	584	12	BG442607	BG442607 GA_Ea001
45	243.8	27.2	700	9	AL509053	AL509053 AL509053

ALIGNMENTS

BI933168	715 bp	mRNA	linear	EST 18-OCT-2001
EST53057	tomato flower, 8 mm to preanthesis buds	Lycopersicon		
esculentum	cdna clone cTOC25K8 5' end, mRNA sequence.			
BI933168	GI:16247640			
EST.				
KEYWORDS	tomato.			
SOURCE	Lycopersicon esculentum			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Asteridae; euasterids I; Solanales; Solanaceae; Solanum;			
REFERENCE	1 (bases 1 to 715)			
AUTHORS	van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,			
	Utterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M.,			
	Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.			
TITLE	Generation of ESTs from tomato flower tissue, buds 8 mm -			
JOURNAL	preanthesis			
COMMENT	Unpublished (2001)			
	Contact: CUGI			
	Clemson University Genomics Institute			
	Clemson University			
	100 Jordan Hall, Clemson, SC 29634, USA			
	Email: http://www.genome.clemson.edu/orders/index.html			
	This clone is available through the Clemson University Genomics			
	Institute			
	Seq primer: T3.			


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Db 537 GAACTGCAGAACGATACATGTACTCTCGAGCAAAATAGTGAATGAAAGAGCGCAA 596
Qy 586 C 586
Db 597 C 597

RESULT 3
B0411583
LOCUS
DEFINITION
  GA_Ed0041A08f Gossypium arboreum 7-10 dpa fiber library Gossypium
  arboreum cDNA clone GA_Ed0041A08f, mRNA sequence.
ACCESSION
  B0411583
VERSION
  B0411583.1 GI:21099270
KEYWORDS
  EST.
SOURCE
  Gossypium arboreum.
ORGANISM
  Gossypium arboreum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE
  1 (bases 1 to 656)
  Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
  ,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  An integrated analysis of the genetics, development, and evolution
  of the cotton fiber
  Unpublished (2000)
  Contact: Wing RA
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson, SC 29634, USA
  Tel: 864 656 7288
  Fax: 864 656 4293
  Email: rwing@clemson.edu
  Total High Quality bases = 625
  Seq primer: TAATACGACTCATATAGGG
  High quality sequence start: 7
  High quality sequence stop: 656.

FEATURES
    source
    1..656
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    /strain="AKA"
    /cultivar="8400"
    /db_xref="taxon:29729"
    /clone="GA_Ed0041A08f"
    /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
    /tissue_type="Fibers isolated from bolls harvested 7-10
    dpa"
    /lab_host="E. coli"
    /note="Vector: pBK-cmv; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT    227 a 146 c 144 g 139 t
ORIGIN

Query Match          35.0%; Score 313.8; DB 14; Length 656;
Best Local Similarity 73.8%; Pred. No. 1.8e-71;
Matches 399; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 46 AAGAACTAGGGAGGAGGAAATAGAGATAAAGAGGATAGAGAACACAACTCGTCAA 105
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Db 45 AAAAAATGGGAATAGGCAAAATCGATTAAGCGGATCGAGAACACCACCTAATCGCAA 104
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 106 GTTACTTCTGCAACACGACCAATGGTCTCTCAAGAAAGCTATGAACTCTGCTCTG 165
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 105 GTTACTTCTGCAAGCGCGCAATGGACTGTCTCAAAAGGCGCTATGAATATCTGTTCT 164
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 166 TGTGATCCGGAAGTTGCCCTCTCATCTCTCCACTCGTGCCTCTCTATGAGTACGCC 225
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 165 TGTGATCTGAGGTGGTCTCATAGTCTCTCCAGCCGTCGCGCTCTATGAATGCT 224
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 226 AACACAGTGTAGGGGTACAAATTAAGAGTACAAAGAAAGTGTTCGATGCCCTGAC 285
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 AACACAGTGTAGGAGCAACAATTAAGAGATACAAAGAAAGTGTTCGATGCCACAACT 284
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 286 CCTCCTTCCTCACCGAAGCTAATACTCAGTACTATCAGCAAGAGCGCTCTAAGCTTCGG 345
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Db 285 CCAGGGTCTGTGGTGAAGCCCAACATTTCAGTTCTTACCAGCAAGCAACCAACCCGA 344
  || || || || || || || || || || || || || || || || || || || || ||
Qy 346 AGGAGATTCGAGATATTCAGAAATTCAGATATTCAGTGGGGAATCATTGGTTCC 405
  || || || || || || || || || || || || || || || || || || || || ||
Db 345 CGACAAATTCGTGATGTTTCAGAACATGACAGGAGCATATCTTGGAGAGGCTCTGAGCTCA 404
  || || || || || || || || || || || || || || || || || || || || ||
Qy 406 TTGAACTTCAAGGAACCTCAAAACCTTAGAAGGACGCTTTGAAAAAGCAATCAGCCGTGTC 465
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 405 TTGACCTTTAAGGAACCTCAAGAACCTTGAAGCGAGCTGGAGAAAGGCAATTTGTAGAATC 464
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 466 CGCTCAAAAAAGATCAGCTGTTAGTGGCAGAGATAGATATATGACAGAGAGGGAATG 525
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Db 465 AGATCCAAAAAGACGAATTTACTGTTTGGAGAAATTTGGATTCATGCAAAAGAGGGAAGTT 524
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Qy 526 GAGTTGCAACACAATAACATGTACTGCGAGCAAGATAGCCGAAGGCGCAGATTGAAT 585
  || || || || || || || || || || || || || || || || || || || || ||
Db 525 GAAGTGCAGACGATAACATGTACTGCGAGCAAAATAGCTGAAATGAAGAGCGCAA 584
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Qy 586 C 586
Db 585 C 585

RESULT 4
B1311095
LOCUS
DEFINITION
  B1311095 EST5312845 GSD Medicago truncatula cDNA clone pGESD9N6 5' end,
  mRNA sequence.
ACCESSION
  B1311095
VERSION
  B1311095.1 GI:14985422
KEYWORDS
  EST.
SOURCE
  barrel medic.
ORGANISM
  Medicago truncatula
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
  Medicago.
REFERENCE
  1 (bases 1 to 748)
  Grusak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T., Cho
  ,J. and Fraser,C.W.
  ESTs from developing reproductive tissues of Medicago truncatula
  Unpublished (2001)
  Contact: Michael A. Grusak
  USDA/ARS Children's Nutrition Research Center
  Baylor College of Medicine
  1100 Bates Street, Houston, TX 77030-2600, USA
  Tel: 713-798-7044
  Fax: 713-798-7078
  Email: mgrusak@bcm.tmc.edu
  B397950e
  TIGR sequence name: MTPAP75TK
  More information is available at: www.medicago.org
  Seq primer: SKmod (CTA gAA CTA gtg gat CC).
  Location/Qualifiers
    1..748
    /organism="Medicago truncatula"
    /cultivar="A17"
    /db_xref="taxon:3880"
    /clone="pGESD9N6"
    /clone_lib="GSD"
    /tissue_type="immature seeds"
    /dev_stage="immature seeds, 11 to 19 days after
    pollination"
    /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
    XhoI; Immature seeds, collected from pods ranging in age
    from 11 to 19 days after pollination, were harvested from
    greenhouse-grown plants. Seeds were removed and
    separated from pod walls and were immediately frozen in
    liquid nitrogen. Seeds throughout the age range were
    pooled for mRNA extraction. cDNA was prepared from polyA+
    enriched RNA. The cDNA was directionally ligated into
    the Unizap XR vector from Stratagene and packaged using
```

Gigapack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-zap
phage using Ex-assist helper phage and propagated in
XL0LR cells."

BASE COUNT	258 a	136 c	161 g	193 t	
ORIGIN					
Query Match	34.98;	Score 312.4;	DB 13;	Length 748;	
Best Local Similarity	69.2%;	Pred. No. 4.2e-71;			
Matches 462;	Conservative	0;	Mismatches 191;	Indels 15;	Gaps 2;
QY	46	AAGAACTAGGAGAGGAAATAGAGATAAAGAGATAGAGAACACACAAATCGTCAA	105		
Db	83	AAGAAATGGAAGAGGAAATTAAGATCAAGAGATTGAACACACTACCAATAGGC	142		
QY	106	GTTACTTTCTCAACACGCGCAATGGTCTTCTCAAGAAGCTTATGAACCTCTCTG	165		
Db	143	GTCACTTTTCAACACGCGCAATGGATGTTGAAGAAGCTTATGAATATCCGTTCT	202		
QY	166	TGTATGCCGAAGTTCCTCGTCATCTCTCCACTCGTGGCGTCTCTATGAGTAGCG	225		
Db	203	TGTATGCCGAAGTTCCTGTTCTCTCCACTCGCGGTCTGTTGATGAGTAGCG	262		
QY	226	AACACAGCTGTAGGGGTACAAATCAAGAGTACAAGAAGCTTGTCCGATGCCCTCA	285		
Db	263	AACACAGCTGTAGAGCAATCTCAAGAGTACAAGAAGCATGTGCTCTCCACTAAC	322		
QY	286	CCTCCTTCGTCACCGAAGCTAATCTCAGTACTATCAGCAGAGAGCCCTTAAGCT	345		
Db	323	GCAGAATCTGTATCTGAAGCTAATACCCAGTTTTACCAGCAAGAATCATCCAA	382		
QY	346	AGGCAGATCCGATATTCAGAAATCAATAGGCATATTTGTTGGGAATCACTTGT	405		
Db	383	AGACAGATTCGATATTCAGAAATCTAATACACACATCTTGGTGAAGCTCTAGAT	442		
QY	406	TGAACTTCAAGGAATCAAAACCTAGAAAGCAGTCTTTGAAAGGAATCAGCCGT	465		
Db	443	CTAAGTCTCAAGAACTGAAGAATCTTGAAGGTAGATTGGAGAAAGGTTTAAG	502		
QY	466	CGCTCAAAAGAAAGTACGTGTAGTGGCAGAGATAGATATATGAGAGAGGAAAT	525		
Db	503	AGATCTAGAAAGCATGAGACTTGTGTTGCTGATGGAGTTTCATGCAAAAGCG	562		
QY	526	GAGTTGCAACACAATAACATGTACCTCGCAGCAAGATAGCCGAAGCGCCAGAT	585		
Db	563	GAGCTGCAAAACCAATAACAATATCTACGGGCTAAGATAGCGGAACATGAGA	616		
QY	586	CGGACACGAGCAATCGAGTGTGATACAGGGACGACAGTTTACGAATCCGTTAT	645		
Db	617	GCTCAACAACAGCAACATAATTTGATGCCAGATCAAAACAATGTTGATCAT	676		
QY	646	TCTCATGACGATCGCAGCATTAATTAATCGAACTATATTCGGTGAACCTTCTT	705		
Db	677	TC-----ATCACAGCATATGACCAAAATTTCTTCCGGTAAATCTTCTTGG	727		
QY	706	AATCAGCA	713		
Db	728	GATCAGCA	735		
RESULT 5					
AW277843					
LOCUS					
DEFINITION	sf87d01.y1 Gm-cl019 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl019-3098 5', similar to SW:AGL5_ARATH P29385 FLORAL HOMEOTIC PROTEIN AGL5. ;, mRNA sequence.				
ACCESSION	AW277843				
VERSION	AW277843.1				
KEYWORDS	EST.				
SOURCE	soybean.				
ORGANISM	Glycine max				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 624)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna
, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
, R., Waterston, R. and Wilson, R.
Public Soybean EST Project

Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1024 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 446.

Location/Qualifiers
1. .624
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl019-3098"
/clone_lib="Gm-cl019"
/tissue_type="Immature seed coats of greenhouse grown
plants"

/lab_host="DH10B (Gibco BRL)"
/note="Vector: pSPORT1 (Life Technologies); Site_1: Not I;
Site_2: Sal I; This cDNA library was constructed from mRNA
isolated from immature seed coats (200-300 mgs) of
greenhouse grown plants. The library was prepared using
the Life Technologies psuperScript cDNA library
construction kit. Complementary DNA was synthesized from
mRNA using a poly (dT) sequence with a Not I restriction
site. Sal I linker adapters were ligated to the
blunt-ended cDNA fragments followed by Not I digestion.
The cDNA fragments were directionally cloned into the Not
I-Sal I restriction site of the pSPORT1 vector. The
ligated cDNA fragments were transformed into E.coli
ElectroMax DH10B host cells (Gibco BRL). This library was
constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
BASE COUNT 210 a 124 c 145 g 142 t 3 others

Query Match	34.8%;	Score 311.6;	DB 10;	Length 624;	
Best Local Similarity	71.1%;	Pred. No. 6.6e-71;			
Matches 410;	Conservative	0;	Mismatches 167;	Indels 0;	Gaps 0;
QY	3	ATCAATGGAGAGGTGGAGTAGTCACGACGACAGAGTAGCAAGAACTAGGAGAGG	62		
Db	24	AACCATGGAGGATCCAAATCAAGCTCCAGAGCGCTTCTCAGAGAAATGGAGAGG	83		
QY	63	GAAATAGAGATAAAGAGGATAGAGAACACACAAATCGTCAAGTTACTTTCTGCA	122		
Db	84	GAGATTGAAATCAACCGGATCGAGAACACCAACCAATAGGCAAGTCACCTTCTG	143		
QY	123	ACGCAATGGCTTCTCAGAAAGCTTATGAACCTCTCTGTGTGATGCCGAAGTTGC	182		
Db	144	CCGAACCGTTGCTGAAAAAGCTTATGAATATATCATGTTCTGTGTGATGCTGAG	203		
QY	183	CCTGCTATCTTCTCCACTCGTGGCGGCTCTATGAGTACGCCCAACAGTGTGAGGG	242		
Db	204	CCTGTGCTCTTCAACCCGTTGGCGGTTGTTGATGATGCCAACACAGTGTTAGGG	263		
QY	243	TACAAATGAAAGGTACAGAAAGCTTGTTCGATGCCGTCAACCCCTCTTCGTACCG	302		
Db	264	CACATTTAGAGGTACAAAGAGGCAAAATGCTGCTCTCAAACGCCAGAAATCGTAT	323		

QY	303	ACGTTAATCTACTAGTCTACTATCATGCAAGAAGCCCTCTTAAGCTTTCGGAGGCGAGATTCGAGATAT	362
Db	324	AGCTTAACACAGAGTTTACCAGAGAGTGTCATCCAAATTTGAGAACACAAATTCGAGATAT	383
QY	363	TCAGAATTCAAATAGGCATATTTGTTGGGAATCACTTGGTTCCCTTGAACCTCAAGGAAT	422
Db	384	TCAGAAATCTAACAGGACATCCCTTGGTGAAGCACTTGGTTCTCTGTAGCTCTCAAGGAAT	443
QY	423	CAAAACCTAGAGGACCTCTTTGAAAAAGGAATCAGCCGTGTCCTCCCAAAAAAGAAATGA	482
Db	444	AAAGAACCTCGAGGTAGATTGGAGAAAGATTAAAGCAGAGTTAGATCTAGAAGCATGA	503
QY	483	GCTGTTAGTCGACAGATAGATATATATCCGAAGAGGAAATGGAGTTGCAACACAATAA	542
Db	504	NACATTTGTTCTGATGTGGAGTTTCATGCANAAAGCGGAAATTCAGCTGCANAAACCAA	563
QY	543	CATGTACCTCGCAGCAAGATAGCGAAGGCGCCAGA	579
Db	564	CAATTATCTCGAGCTAGATAGCTGAACATGAGAGA	600
RESULT	6		
LOCUS	BI310910		
DEFINITION	EST5312660 GESD Medicago truncatula cDNA clone pGESD9K22 5' end,		
ACCESSION	BI310910	754 bp	mRNA linear EST 20-JUL-2001
VERSION	BI310910.1	GI:14985237	
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.		
AUTHORS	1 (bases 1 to 754) Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho, J., and Fraser, C.M.		
TITLE	ESTs from developing reproductive tissues of Medicago truncatula		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Michael A. Grusak USDA/ARS Children's Nutrition Research Center Baylor College of Medicine 1100 Bates Street, Houston, TX 77030-2600, USA Tel: 713-798-7044 Fax: 713-798-7078 Email: mgrusak@bcm.tmc.edu B397765e		
FEATURES	TIGR sequence name: MTPAN71TK More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gat CC).		
SOURCE	Location/Qualifiers 1..754 /organism="Medicago truncatula" /cultivar="A17" /db_xref="taxon:3880" /clone="pGESD9K22" /clone_lib="GESD" /tissue_type="immature seeds" /dev_stage="Immature seeds, 11 to 19 days after pollination" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature seeds, collected from pods ranging in age from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using GigaPack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap		

AUTHORS Grusak,M.A., Samak,D., Town,C.D., Van Aken,S., Utterback,T., Cheung ,F. and Fraser,C.M.
TITLE ESTs from late stage developing seeds of Medicago truncatula
JOURNAL Unpublished (2002)
COMMENT Contact: Grusak, M.A.
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713 798 7044
Fax: 713 798 7078
Email: mgrusak@bcm.tmc.edu
TIGR sequence name: WPA030TK More information is available at:
www.medicago.org
Seq primer: Skmod (CTA GAA CTA gty gAT CC).
FEATURES
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/organism="Medicago truncatula"
/cultivar="A17"
/db_xref="taxon:3880"
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/tissue_type="Immature seeds"
/dev_stage="25 to 35 days after pollination"
/lab_host="XL0LR"
/note="vector: pbluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature seeds, collected from pods ranging in age from 25 to 35 days after pollination, were harvested from greenhouse-grown plants. Seed were removed and separated from pod walls and immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in XL0LR cells."
BASE COUNT 215 a 115 c 136 g 170 t
ORIGIN
Query Match 33.8%; Score 302.4; DB 14; Length 636;
Best Local Similarity 71.7%; Pred. No. 1.7e-68;
Matches 396; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 53 TAGGAGAGGGAATACAGATAAGAGATAGAGAACACAAATCTCAAGTTACTT 112
DB 2 TGGGAAGAGGAAAATTGAAATCAAGAGGATTGTAACACTACCAATAGCGCAAGTCAC 61
QY 113 TCTGCAACGAGCGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTGTGTGATG 172
DB 62 TTTCGCAACGAGCGCAATGGATTGTTGAAGAAAGCTTATGAATATCTCTTCTGTGTGATG 121
QY 173 CGAAGTTGCCCTCGTCATCTTCTCACTCGCGGCTCTATGATGATGACGCAACAACA 232
DB 122 CCGAAGTTGCTCTTGTCTTCTCACTCGCGGCTGTGTGATGATGATGCAACAACA 181
QY 233 GTGTGAGGGTACAATGAAGGTCAAGAAAGCTTGTTCGATGCGCTCAACCCCTCTT 292
DB 182 GTGTGAGCAACTATTGAAGGTACAAAAGCATGTCTGCTTCCACTAAGCGAGAAT 241
QY 293 CGTCCAGCAAGCTAATCTAGTACTATFACAGAAAGCGCTTAAGCTTCGGAGGACGA 352
DB 242 CTGTATCTGAAGCTAATACCCAGTTTACCAGCAAGAATCATCCAAATTTGAGAAGACGA 301
QY 353 TTCGAGATATTCAGAAATCAATAGGCATATTGTTGGGAATCAGTTGGTTCCTTGAAC 412
DB 302 TTCGAGATATTCAGAAATCAATAGACATCTTGGTGAAGCTCTAGAGTCTTAGTC 361
QY 413 TCAAGGAACCTAAAACCTVAGAGGAGCTCTTGAAGAAAGAAATFACGCCGTCCGCTCCA 472
DB 362 TCAAGAACTGAAGAACTCTTGAAGGTAGATTGAGAAAGGTTTAAAGCAGAGTTAGATCTA 421
QY 473 AAAGAAAGAGCTGTAGTGGCAGAGATAGATATATGACAGAGAGGGAATGAGTTGC 532

DB 422 GAAAGCATGAGACTTTTGTGTGTGAGTTCTGCAAAAGCGGAAATTTGAGCTGC 481
QY 533 ACACAAATACATGTACCTGCGAGCAAGATAGCCGAGCGCCAGATTGAATCCGAGCC 592
DB 482 AAACCATACCAATTTATCTACGGCTAAGATAGCGGAACATGAGAGAGCTCAACAACAGC 541
QY 593 AGCAGGAATCGA 604
DB 542 AACATAATTGA 553
RESULT 8
BE659918 656 bp mRNA linear EST 06-SEP-2000
LOCUS 1299.GmaxSC Glycine max cDNA, mRNA sequence.
DEFINITION BE659918
ACCESSION BE659918
VERSION BE659918.1 GI:9985912
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 656)
AUTHORS Harris,N., Chapman,B.P. and Gijzen,M.
TITLE Gene expression in developing soybean seed coats
JOURNAL Unpublished (2000)
COMMENT Contact: Gijzen M
Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: gijzenm@agr.ca.
FEATURES
source
1. .656
/organism="Glycine max"
/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_lib="GmaxSC"
/tissue_type="Seed coats"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from polyA+ enriched mRNA from green seed coats in mid to late developmental stage , average fresh weight 250 mg per seed. Traces of pod and embryo tissue also present. Complementary DNA was synthesized from mRNA using an XhoI-poly(dT) linker-primer. EcoRI adapters and the products were digested blunt-ended cDNA fragments and the products were digested with XhoI for directional cloning into lambda ZAP Express vector. This lambda library was amplified once using E. coli host strain XLI Blue MRF'. Inserts were then subcloned by mass excision using ExAssist helper phage for conversion into phagemid vector pBK-CMV in E. coli host strain XL0LR."
BASE COUNT 225 a 129 c 148 g 152 t
ORIGIN
Query Match 33.5%; Score 299.8; DB 10; Length 656;
Best Local Similarity 70.9%; Pred. No. 8.2e-68;
Matches 411; Conservative 0; Mismatches 168; Indels 1; Gaps 1;
QY 1 GGATCAATGGAGGAGGTGGGAGTAGTCCAGCAGCAGAGAGTAGCAAGAACTAGGGAGA 60
DB 44 GCACCATGGNGGATCCAAATCAAGCTCCAGAGCGTCTTCTCAGAAGAAAATGGGA 103
QY 61 GGGAAATAGAGATAAGAGGATAGAGAACACAAATCGTCAAGTTACTTCTGCARA 120
DB 104 GGGAAAGTTGAATCAAAACGGATCGAGAACACACCACATAGGCAATGACCTTCGTGCAAG 163
QY 121 CGACGCAATGCTCTCTCAAGAAAGCTTATGAACCTCTCTGTTGTGTGATGCCGAAGTT 180


```

Db 164 GCGCCGAACGGTTTGTGTAAGAAAGCTTATGAATATCAGTTCTGTGTGATGCTGAAGTT 223
Qy 181 GCGCCGTCATCTTCCACTCGTGGCGTCTCTATGAGTAGCCACACACAGTGTGAGG 240
Db 224 GCGCTTGTGTTCTCTCAACCGTGGCGGTTGTATGAGTATGCCAACACAGTGTGAGG 283
Qy 241 GGTACAATGAAAGTACAGAAAGCTTGTTCGGATGCGCTCAACCTCTCCGTCACC 300
Db 284 GCCACTATTGAGAGTACAGAAAGCAAAATGCTGCTCTCAACGAGAAATCGTATCT 343
Qy 301 GAAGCTATACTACGACTATACAGCAAGAGCTCTAAGCTTCGGAGGCGAGATTCGAGAT 360
Db 344 GAAGCTACACACAGCTTTTACAGCAAGAGTATCTCAAAATTTGAGAGACAAATTCGAGAT 403
Qy 361 ATTCAGAAATCAAAATGAGCATATTTGGGGAATCACTTGGTTCCTTGAATCTCAAGGAA 420
Db 404 ATTCAGAAATCTAAACAGGCACATCTTGTGTGAAGCACTTGGTTCTCTGAGTCTCAAGGAA 463
Qy 421 CTCAAAACCTTAGAAGGACGCTTTGAAAAGGAATCAGCGCTGTCGCTCCAAAAGAAAT 480
Db 464 CTAAGAACCTCGAGGGTAGATTGGAGAAAGGATTAAAGCAGAGTTAGATCTAGAAGCAT 523
Qy 481 GAGCTGTAGTGGCAGACATAGATATATGACAGAGAGGAATGAGTTGCAACACAAAT 540
Db 524 GAAACATTTGTTGTGATGTGAGTTCATGCAAAAGAGCGGGAATTTGAGCTGCAAAACCCAC 583
Qy 541 AA-CATGTACTCTCGCAGCAAAATAGCCGAGCGGCCGAG 579
Db 584 AACCANTATCTCGAGCTAGATAGCTGAACATGAGAGA 623

RESULT 9
AW277299
LOCUS
DEFINITION
  AW277299 548 bp mRNA linear EST 02-DEC-2001
  sF80e05.y1 Gm-cl019 Glycine max cdna clone GENOME SYSTEMS CLONE ID:
  Gm-cl019-2457.1 similar to SW:AGL5-ARATH P29385 FLORAL HOMEOTIC
  PROTEIN AGL5.1; mRNA sequence.
ACCESSION
  AW277299
VERSION
  AW277299.1 GI:6665849
KEYWORDS
  EST.
SOURCE
  soybean.
ORGANISM
  Glycine max
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
  Glycine.
REFERENCE
  1 (bases 1 to 548)
  Shoemaker,R., Keim,P., Vodkin,L., Erpelnding,J., Coryell,V., Khanna
  ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
  Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
  ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
  ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
  ,R., Waterston,R. and Willson,R.
  Public Soybean EST Project
  Unpublished (1999)
  Contact: Shoemaker R/Public Soybean EST Project
  Public Soybean EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@wustl.wustl.edu
  This clone is available through: ResGen, Invitrogen Corp. 2130
  South Memorial Parkway Huntsville, AL 35801 For further information
  call: (800)-533-4363 or contact via email: ccu@resgen.com
  Insert Length: 949 Std Error: 0.00
  Seq primer: -4ORP from Gibco
  High quality sequence stop: 438.
  Location/Qualifiers
  1..548
  /organism="Glycine max"
  /db_xref="taxon:3847"
  /clone="GENOME SYSTEMS CLONE ID: Gm-cl019-2457"

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/clone_lib="Gm-cl019"
/tissue_type="immature seed coats of greenhouse grown
plants"
/lab_host="DH10B (Gibco BRL)"
/notes="Vector: pSPORT1 (Life Technologies); Site_1: Not I;
Site_2: Sal I; This cDNA library was constructed from mRNA
isolated from immature seed coats (200-300 mgs) of
greenhouse grown plants. The library was prepared using
the life Technologies pSuperScript cDNA library
construction kit. Complementary DNA was synthesized from
mRNA using a poly (dT) sequence with a Not I restriction
site. Sal I linker adapters were ligated to the
blunt-ended cDNA fragments followed by Not I digestion.
The cDNA fragments were directionally cloned into the Not
I-Sal I restriction site of the pSPORT1 vector. The
ligated cDNA fragments were transformed into E.coli
ElectroMax DH10B host cells (Gibco BRL). This library was
constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
BASE COUNT 187 a 107 c 128 g 126 t
ORIGIN

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Query Match 33.4%; Score 299; DB 10; Length 548;
Best Local Similarity 73.8%; Pred. No. 1.3e-67;
Matches 380; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Qy 56 GGAGAGGGAATAGAGATAAGAGGATAGAGACACAAATCGTCAAGTTACTTTCT 115
Db 1 GAAGAGGGAAGATTGAATCAACGGATCGAGACACACCAATAGGCAAGTCACCTTCT 60
Qy 116 GCAAGCGAGCAATGCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTGTGTGATCGG 175
Db 61 GCAAGCGCGCAACGGTTGCTGAAAAGAGCTTATGAATATCAGTTCTGTGTGATGCTG 120
Qy 176 AAGTTGCCCTCGTCATCTTCTCCACTCGTGGCGGTCTCTATGAGTACGCCCAACACAGTG 235
Db 121 AAGTTGCCCTTGTGTCTTCTCAACCGTGGCGGTTGTATGAGTATGCCAACACAGTG 180
Qy 236 TGAGGGGTACAATTGAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCTCTCCTCG 295
Db 181 TTAGGGCCACTATTGAGAGGTACAGAAAGCAATGTGCTTCAACGACGAAATCCG 240
Qy 296 TCACCGAAGCTAATACCTACGACTATCAGCAAGAGCTCTAAGCTTCGGAGGAGATTC 355
Db 241 TATCTGAAGCTAACACACAGTTTACCAGCAAGAGTCATCCAAATTGAGAAGACAAATTC 300
Qy 356 GAGATATTCAGAAATCAAAATAGGCATATTTGTTGGGAATCAGTGTGTTGTTGAATTC 415
Db 301 GAGATATTCAGAAATCTAAACAGGCACATCTTGGTGAAGCACTTGGTTCTCTGAGTCTCA 360
Qy 416 AGGAACTCAAAAACCTTAGAAGGACGCTTTGAAAAGGAATCAGCGGTCCGCTCCAAA 475
Db 361 AGGAACTAAAGAACCTCGAGGGTAGATTGGAGAAGAGATTAAAGCAGAGTTAGATCTAGAA 420
Qy 476 AGAATGAGCTGTTAGTGGCAGAGATAGATATATGCAAGAGAGGGAATGAGTTGCAAC 535
Db 421 AGCATGAAACATTTGTTGCTGATGTGGATTCTCAAAAGCGGAGATTGAGCTGCAAA 480
Qy 536 ACAATAAGATGTACCTCGCAGCAAGAGATAGCCGAA 570
Db 481 ACCACAACAATTTCTGCGAAGTAAAGATAGCTGAA 515

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RESULT 10
BE434089
LOCUS
DEFINITION
  BE434089 548 bp mRNA linear EST 18-MAY-2001
  EST405167 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
  clone cLEG14H7, mRNA sequence.
ACCESSION
  BE434089
VERSION
  BE434089.1 GI:9431932
KEYWORDS
  EST.
SOURCE
  tomato.
  Lycopersicon esculentum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 548)
AUTHORS Alcalá, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.

TITLE Generation of ESTs from tomato fruit tissue, breaker stage
JOURNAL Unpublished (2000)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES Location/Qualifiers
Source 1..548
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="GLE14H7"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/note="Vector: pBluescriptSKMcuadapt; Site_1: EcoRI; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
BASE COUNT 199 a 101 c 130 g 118 t

Query Match 33.0%; Score 295.8; DB 10; Length 548;
Best Local Similarity 74.0%; Pred. No. 8.9e-67;
Matches 375; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 46 AGAACTAGGGAGAGGGAATAGAGATAAGAGGATAGAGACACAACTCGTCAA 105
DB 42 AGAACTAGGAGGGGAAATAGAGATCAAAAGGATCGAAACACGACGATCGCAA 101
QY 106 GTTACTTCTGCAACGACGCAATGGTCTCTCAAGAAAGCTTATGAATCTCTCTTTG 165
DB 102 GTACATCTCGAGAGCGCAATGGTCTTAAAGAGCTTATGAATGCTCTGCTC 161
QY 166 TGTGATGCGGAAGTGGCTCGTCACTTCTCCACTCGTGGCCGCTCTATCAGTACGCC 225
DB 162 TGTGATGCTGAGGTGGTCTTGGTCTCTCAACAGAGCGACAGCTATGAGTATGCC 221
QY 226 AACACAGTGTGAGGGGTACAAATGAAAGGTACAGAAAGCTTGTTCGATGCCGTCAAC 285
DB 222 AACACAGTGTGAAGCAACAATCGAGAGGTACAGAAAGCATGCTCAGATTCCTCAAC 281
QY 286 CCTCCTTCGTCACCGAAGCTAATCTACGTACTATCAGTAAAGCGCTCTAAGCTTGG 345
DB 282 ACTGTTTCAGTATCCGAGGCAATGCTCAGTATACCAGCAAGAGCTCCAACTGCCG 341
QY 346 AGGAGATTTCAGATATTCAGAAATCAATAGGCATATGTTGGGGAATCACTTGGTTCC 405
DB 342 GCACAAATTTGAAATCTGATCAACCAACAGGACATGATGGGTGAAGCTCTTCTGGA 401
QY 406 TTGAATTCAGAGGAATCAAAACCTAGAGGACGCTCTTGAAGAAAGATCAGCCGTGTC 465
DB 402 ATGAATTCAGAGGAATCAAGAACTCGAGCAAGAAATTTGAAGAAAGGATTTAGCAAAATC 461
QY 466 CGCTCCAAAAAGATGAGCTGTTAGTGGCAGAGATAGAGTATATCGAGAAAGGGAATG 525
DB 462 CGATCCAAAAAGATGAGCTGTTGTTGCTGAATTTGAGTATATCAGAAAGGGAAGTT 521
QY 526 GAGTTGCAACACATAACATGTACCTG 552
DB 522 GATTTCACAAACACATCAGTACCTG 548

RESULT 11
BI272847
LOCUS
DEFINITION NF097G09FL1F1071 Developing flower Medicago truncatula cDNA clone
NF097G09FL 5', mRNA sequence.
ACCESSION BI272847
VERSION BI272847.1 GI:14882522
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 555)
AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
JOURNAL Unpublished (2001)
COMMENT Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 555 Std Error: 0.00
Plate: 097 row: G column: 09
Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES Location/Qualifiers
Source 1..555
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF097G09FL"
/clone_lib="Developing flower"
/tissue_type="Developing flowers"
/dev_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and in early transition into pods."
/note="Vector: Lambda Zap; cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

BASE COUNT 194 a 92 c 120 g 143 t 6 others
ORIGIN
Query Match 32.8%; Score 292.2; DB 13; Length 555;
Best Local Similarity 72.8%; Pred. No. 7.8e-66;
Matches 372; Conservative 0; Mismatches 139; Indels 0; Gaps 0;
QY 46 AAGAACTAGGAGGGGAAAAATAGAGATAAGAGGATAGAGACACAACTCGTCAA 105
DB 45 AAGAAATGGAGAGAGGAAAAATGAATCAATCAAGAGGATGAAACACTACCAATAGGCAA 104
QY 106 GTTACTTCTGCAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAATCTCTGCTTTG 165
DB 105 GTCATTTTTTCAACGACGCAATGGATGTTGAAGAAAGCTTATGAATATTCGCTTCTT 164
QY 166 TGTGATGCCAAGTTGCCCTCGTCATCTTCCACTCGTGGCCGCTCTATCAGTACGCC 225
DB 165 TGTGATGCCAAGTTGCTGTTGTTCTTCCACTCGCGTCTGTTGATGAGTATGCC 224
QY 226 AACAACTGTGTAGGGGTACAAATGAAAGGTACAGAAAGCTTGTTCGATGCCGTCAAC 285

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||||| 225 AACACAGTGTAGAGCAACTATTGAAAGTCACAAAAGCATGTGCTTCCACTAAC 284
QY 286 CTCCTCTCGTCCAGCAAGCTAATCTAGTACTATCAGCAAGAGCCTCTAAGCTTCGG 345
Db 285 GCAGAACTGTATCTGAAAGCTAATACCCAGTTTACCAGCAAGAAATCATCCAAATTGAGA 344
QY 346 AGGCAGATTCGAGATTCAGAAATTCAAATAGCAATATCTGTTGGGAATCACTTGGTTCC 405
Db 345 AGACAGATTCGAGATTCANAACTTAAATAGACACATCTCTGTTGAAGCTCTAGGATCT 404
QY 406 TTGAATCTCAAGGAACCTCAAAACCTAGAGGACGCTTTGAAAAGGAATCAGCCGTGTC 465
Db 405 CTAAGTCTCAAGAACTAGAAATCTTGAGGTAGATTGGAGAAAGGTTAAAGCANAGTT 464
QY 466 CGCTCCAAAAGCAATGAGCTGTAGTGGCAGAGATAGAGTATATGCAGAGAGGGAATG 525
Db 465 ANATCTANAAGCATGANACTTTGTTGCTGATGTGGAGTTCATGCAAAAACGCGAAAT 524
QY 526 GAGTTGCAACACAATAACATGTACCTGCGAG 556
Db 525 GAGCTGCAAAACCAACAATATCTACGGG 555

RESULT 12
BE433121
LOCUS
DEFINITION BE433121 538 bp mRNA linear EST 18-MAY-2001
ACCESSION EST399650 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
VERSION Clone CL6G12616, mRNA sequence.
KEYWORDS BE433121.1 GI:9430964
SOURCE tomato.
ORGANISM Lycopersicon esculentum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Rønning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
, S.D.
Generation of ESTs from tomato fruit tissue, breaker stage
Unpublished (2000)
Contact: CUGI
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
source
Location/Qualifiers
1..538
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEGI2G16"
/tissue_type="tomato breaker fruit, TIGR"
/dev_stage="breaker"
/lab_host="SOLR"
/notes="vector: pluescriptSKmCUadapt; Site_1: EcoRI;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 197 a 98 c 128 g 115 t
ORIGIN

Query Match 32.4%; Score 290.6; DB 10; Length 538;
Best Local Similarity 74.0%; Pred. No. 2e-65;
Matches 368; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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QY 46 AGAAACTAGGGAGAGGAAAATAGAGATAAAGAGGATAGAGAACACAAACATCGTCAA 105
Db 42 AGAAACTAGGAGGGGAAAATAGATCAAAAGGATCGAAACACGACGATCGACAA 101
QY 106 GTTACTTTCTGCAACAGCACAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGCTTG 165
Db 102 GTAACATCTGCAAGAGCGCAATGGTTGCTTAAAAAGGCTTATGAATGTCTGTGCTC 161
QY 166 TGTGATCCCGAAGTTGCCCTCGTCATCTTCTCCACTCGTGGCCCTCTATGAGTACGCC 225
Db 162 TGTGATGCTCAGGTTGCTTGGTTGCTCTTCTCAACAGAGCGCAGACTCTATGAGTATGCC 221
QY 226 AACAAACAGTGTGAGGGGTACAAATTAAGAGGTACAAAGAAAGCTTGTTCGATGCCGTCAA 285
Db 222 AACAAACAGTGTGAAGCAACAATCGAGAGGTACAAAGAAAGCATGCTCAGATTCTCTCAAA 281
QY 286 CTCTCTCCCTCACCAGAAAGCTTAATCTCAGTACTATCAGCAAGAGGCTCTTAAGCTTCGG 345
Db 282 ACTGGTTCAGTATCCGAGGCCAATGCTCAGTATTACCAGCAAGAGGCTTCCAAACTGCGC 341
QY 346 AGGCAGATTCGAGATATTCAGAAATTCAAATAGGCATATTTTGGGGAATCACTTGGTTCC 405
Db 342 GCACAAATTTGAAATCTGATGAACCAACAGGAACATGATGGGTGAAGCTCTTGTCTGGA 401
QY 406 TTGAATCTCAAGGAACCTCAAAACCTAGAGGAGCGTCTTTGAAAAGGAATCAGCCGTGTC 465
Db 402 ATGAAACTCAAGAACTGAAGAATCTGGACAAAGAAATTTGAAAAGGATTCACAAATC 461
QY 466 CGCTCCAAAAGAAATGAGCTGTAGTGGCAGAGATAGAGTATATGCAGAGAGGGAATG 525
Db 462 CGATCCAAAAGAAATGAGCTGTGTTGCTGAAATTTAGTATATGCAGAGAGGGAAGTT 521
QY 526 GAGTTGCAACACAATAA 542
Db 522 GATTACACAACAACA 538

RESULT 13
BE445079
LOCUS
DEFINITION BE445079 776 bp mRNA linear EST 15-MAR-2001
ACCESSION GA_Ea0026K23f Gossypium arboreum 7-10 dpa fiber library Gossypium
VERSION arboreum cDNA clone GA_Ea0026K23f, mRNA sequence.
KEYWORDS BE445079.1 GI:13354731
SOURCE EST.
ORGANISM Gossypium arboreum
REFERENCE Gossypium arboreum
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 776)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 768.
Location/Qualifiers
1..776
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0026K23f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
FEATURES
source

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VERSION BG444639.1 GI:13354291

KEYWORDS EST.

SOURCE Gossypium arboreum.

ORGANISM Gossypium arboreum.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

REFERENCE 1 (bases 1 to 892)

AUTHORS Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry D., Wood,T.C., Leslie,A. and Wilkins,T.A.

TITLE An integrated analysis of the genetics, development, and evolution of the cotton fiber

JOURNAL Unpublished (2000)

COMMENT Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TAATAGCTACTATAGGG

High quality sequence start: 6

High quality sequence stop: 685.

FEATURES

source

1..892

/organism="Gossypium arboreum"

/strain="AKA"

/cultivar="8400"

/db_xref="taxon:29729"

/clone="GA_Ea0025A08f"

/clone_lib="Gossypium arboreum 7-10 dpa fiber library"

/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"

/lab_host="E. coli"

/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 303 a 161 c 192 g 223 t 13 others

Query Match 32.1%; Score 288; DB 12; Length 892;

Best Local Similarity 70.8%; Pred. No. 1.1e-64;

Matches 384; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 46 A G A A A C T A G G G A G A G A A A T A G A G A T A A G A G A T A G A G A C A C A C A A A A T C G T C A A 105

DB 89 A A G A G A T G G A G A G A G A A A A T A G A T A A G A G A T C G A A A C A C A C A A A T C G T C A G 148

QY 106 G T T A C T T T C G C A A A C G C G A T G G T T C T C A A G A A G C T T A T G A A C T C T C T G T C T T G 165

DB 149 G T T A C C T T T T G C A A A C G C A G A A T G G C T G C T G A A G A A G C T T A C G A A C T G C A G T C C T G 208

QY 166 T G T G A T C C G A A G T G C C C T C A T C T T C C A C T C G T G C C G C T C T A T A G A T A C G C C 225

DB 209 T G T G A T C T G A A G T G C T C A T G T C T T C C A G T C G A G C C G C T G T A T A G T A C T C C 268

QY 226 A A C A C A G T T G A G G G T A C A A T T A A A G G T A C A A A A G C T T G T T C C G A T C C C G T C A A C 285

DB 269 A A C A C A A C A T A A G T C A C A A T A G A C A G G T A C A A G A G G C T T G C T C A G A T A C T T C T A A C 328

QY 286 C C T C C T T C C G T C A C C G A G C T A A T A C T C A G T A C T A T C A G C A A G A A G C C T C T A A G C T T C G G 345

DB 329 A C A A A C A C T G T T A C T G A A T C A A T G C T C A G T A T T A C A A G A A T C A G C C A A G T T G A G A 388

QY 346 A G G C A G A T T C G A G A T T C A A A T T C A A A T A G G C A T A T T G T G G G A A T C A C T T G G T T C C 405

DB 389 C A C A G A T T C A A T G T T A C A G A A T T C T A C A G G C A C C T A A T G G G A G A T T C C T T G A G T T C C 448

QY 406 T T G A A C T T C A A G A A C T C A A A A C C T A G A A G A G C G T C T T G A A A A G A A T C A G C C G T C 465

DB 449 T T A A C T G T A A A G A G T T A A A C G A G G T A G A A A C A G G C T T G A A A G A G A A T T A C T A G G A T C 508

QY 466 C G C T C C A A A A A G A A T A G A C T G T T A G T G C G A G A T A G A T A T C A G A A G A G G A A A T G 525

DB 509 A G G T C C A A G A A G A C C A A A T G C T A C T A G C T G A A A T A G A G T T T T T G C A G A A A A G G A A A T C 568

QY 526 G A G T T C C A A C A C A A T A A C A T G T A C T T G C G A G C A A A G A T A G C C G A A G C C C A G A T T C A A T 585

DB 569 G A A T T G G A A A A T G A A A G T C T T T G T C T C C G A A C C A A G A T T G C A G A A A T T G A G A G C T T C A G 628

QY 586 C C G G 589

DB 629 C A G G 632

Search completed: February 2, 2003, 12:14:41

Job time : 1633.91 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 06:43:28 ; Search time 50.234 Seconds
(without alignments)
8013.329 Million cell updates/sec

Title: US-09-978-382A-3
Perfect score: 896
Sequence: 1 ggatacaggaggagggtgg.....actgtgtgtttcttcttgcctca 896

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues 793544
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	896	100.0	896	9	US-09-978-729A-3
2	896	100.0	896	9	US-09-981-087A-3
3	896	100.0	896	9	US-09-978-382A-3
4	896	100.0	896	10	US-09-978-740A-3
5	896	100.0	896	10	US-09-978-730-3
6	536.8	59.9	959	9	US-09-978-729A-5
7	536.8	59.9	959	9	US-09-981-087A-5
8	536.8	59.9	959	9	US-09-978-382A-5
9	536.8	59.9	959	9	US-09-978-740A-5
10	536.8	59.9	959	10	US-09-978-730-5
11	196.2	21.9	845	10	US-09-770-445-644
12	166.6	18.6	645	9	US-09-938-842A-1776
13	166.6	18.6	645	9	US-09-853-450-33
14	149.2	16.7	1062	9	US-09-978-729A-1
15	149.2	16.7	1062	9	US-09-981-087A-1
16	149.2	16.7	1062	9	US-09-978-382A-1
17	149.2	16.7	1062	9	US-09-978-740A-1
18	149.2	16.7	1062	10	US-09-978-730-1
19	143.2	16.0	1345	9	US-09-853-450-7

20	142.2	15.9	666	9	US-09-938-842A-2442	Sequence 2442, Ap
21	131.2	14.6	747	9	US-09-853-450-27	Sequence 27, Appl
22	130.4	14.6	5497	10	US-09-916-780A-7	Sequence 7, Appli
23	128.6	14.4	794	9	US-09-853-450-3	Sequence 3, Appli
24	127.6	14.2	753	9	US-09-853-450-29	Sequence 29, Appl
25	127.6	14.2	768	9	US-09-853-450-5	Sequence 5, Appli
26	125.8	14.0	705	9	US-09-938-842A-2404	Sequence 2404, Ap
27	123.8	13.8	1280	10	US-09-970-624-1	Sequence 1, Appli
28	122.6	13.7	663	9	US-09-853-450-37	Sequence 37, Appl
29	122	13.6	1057	9	US-09-853-450-1	Sequence 1, Appli
30	120.4	13.4	777	9	US-09-938-842A-1873	Sequence 1873, Ap
31	117.2	13.1	779	9	US-09-853-450-9	Sequence 9, Appli
32	110.6	12.3	633	9	US-09-853-450-35	Sequence 35, Appl
33	110.4	12.3	756	9	US-09-938-842A-718	Sequence 718, App
34	108.4	12.1	633	9	US-09-938-842A-1202	Sequence 1202, Ap
35	103	11.5	5171	9	US-09-853-450-42	Sequence 42, Appl
36	102.2	11.4	756	9	US-09-853-450-11	Sequence 11, Appl
37	101.6	11.3	714	9	US-09-853-450-31	Sequence 31, Appl
38	101.4	11.3	5131	9	US-09-853-450-43	Sequence 43, Appl
39	100	11.2	5392	9	US-09-853-450-45	Sequence 45, Appl
40	99.8	11.1	5070	9	US-09-853-450-44	Sequence 44, Appl
41	95.8	10.7	262	10	US-09-878-574-9686	Sequence 9686, Ap
42	94.2	10.5	756	9	US-09-853-450-13	Sequence 13, Appl
43	93.4	10.4	5483	9	US-09-853-450-47	Sequence 47, Appl
44	88.4	9.9	407	10	US-09-878-574-19	Sequence 19, Appl
45	87	9.7	365	10	US-09-878-574-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-978-729A-3
; Sequence 3, Application US/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liliegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978,729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
US-09-978-729A-3

Query Match	100.0%;	Score 896;	DB 9;	Length 896;
Best Local Similarity	100.0%;	Pred. No. 3.5e-257;		
Matches 896;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GGATCAATCGAGGAAGTGGGAGTAGTCAGCCAGAGTAGCAAGAACTAGGGAGA	60	
Db	1	GGATCAATCGAGGAAGTGGGAGTAGTCAGCCAGAGTAGCAAGAACTAGGGAGA	60	
Qy	61	GGCAAAATAGAGATAAAGAGTAGAGAACACACAACAACTCGTCAAGTTACTTTCTGCAAA	120	
Db	61	GGCAAAATAGAGATAAAGAGTAGAGAACACACAACAACTCGTCAAGTTACTTTCTGCAAA	120	
Qy	121	CGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATGCCGAAGTT	180	

121 CGAGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTGCTGTGTGATCCGGAAGTT 180
181 GCCCTCGTCATCTTCTCAACATCGTGGCGCTCTCTATGAGTAGCCCAACAACAGTGTGAGG 240
181 GCCCTCGTCATCTTCTCAACATCGTGGCGCTCTCTATGAGTAGCCCAACAACAGTGTGAGG 240
241 GGTACAATTGAAAGTACAGAAAGCTTGTTCGGATGCGGTCAACCCCTCTCCGTCACC 300
241 GGTACAATTGAAAGTACAGAAAGCTTGTTCGGATGCGGTCAACCCCTCTCCGTCACC 300
301 GAAGCTAATCTAGTACTATATCAGCAAGAAGCTCTAAGCTTCGGAGGAGATTCGAGAT 360
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361 ATTCAGAAATCAATAGGATATATGTTGGGGAATCACTTGGTTCCTTGAACATTCAGGAA 420
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421 CTCRAAAACCTAGAGGAGCTTCTCAAAAAGGAATCAGCCGTGTCGCTCCCAAAAAGAAAT 480
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661 CAGCAATTAATFCGGAATATATTCGGTGAACCTTCTTGAACCGGAATCAGCAATTCCTCC 720
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721 GCCAAGACCAACCTCTCTCAACTGTTGTAACCTCAAAACATGATAACTGTTCTCTCC 780
721 GCCAAGACCAACCTCTCTCAACTGTTGTAACCTCAAAACATGATAACTGTTCTCTCC 780
781 CCTCATAAGATTAAGAGAGACGAGAGTTCATTTTATATTTTATAACGCGACTGTGT 840
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841 ATTCATAGTTTAGGTTCTAATATGATAATAACAAACCTGTTCTTTGCTTCA 896

RESULT 2
US-09-981-087A-3
; Sequence 3, Application US/09981087A
; Patent No. US20020178466A1
; GENERAL INFORMATION:
; APPLICANT: Vanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: Farrandiz, Cristina
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-0009400S
; CURRENT APPLICATION NUMBER: US/09/981,087A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3

LENGTH: 896
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
; OTHER INFORMATION: AGAMOUS-Like 1 (AGL1)
US-09-981-087A-3

Query Match 100.0%; Score 896; DB 9; Length 896;
Best Local Similarity 100.0%; Pred. No. 3.5e-257; Indels 0; Gaps 0;
Matches 896; Conservative 0; Mismatches 0;

QY 1 GGATCAATGAGGAAGGTGGGAGTAGTCAGACGACGAGAGTAGCAAGAACTAGGGAGA 60
Db 1 GGATCAATGAGGAAGGTGGGAGTAGTCAGACGACGAGAGTAGCAAGAACTAGGGAGA 60

QY 61 GGAATAATAGAGATAAAGAGATAGAGAACACAACTCTCAAGTTACTTTCTGCAAA 120
Db 61 GGAATAATAGAGATAAAGAGATAGAGAACACAACTCTCAAGTTACTTTCTGCAAA 120

QY 121 CGAGCAATGCTTCTCAAGAAAGCTTATGAACCTCTCTGCTTGTGTGATGCCGAAGTT 180
Db 121 CGAGCAATGCTTCTCAAGAAAGCTTATGAACCTCTCTGCTTGTGTGATGCCGAAGTT 180

QY 181 GCCTCTGCTCATCTTCTCCACTCGTGGCGCTCTATGAGTAGCCCAACAACAGTGTGAGG 240
Db 181 GCCTCTGCTCATCTTCTCCACTCGTGGCGCTCTATGAGTAGCCCAACAACAGTGTGAGG 240

QY 241 GGTACAATTGAAAGTACAGAAAGCTTGTTCGGATGCGGTCAACCCCTCTTCCGTCACC 300
Db 241 GGTACAATTGAAAGTACAGAAAGCTTGTTCGGATGCGGTCAACCCCTCTTCCGTCACC 300

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Db 301 GAAGCTAATCTAGTACTATCAGCAAGAAGCTCTAAGCTTCGAGGAGAGATTCGAGAT 360

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Db 361 ATTCAGAAATCAATAGGATATATGTTGGGGAATCACTTGGTTCCTTGAACCTTCAGGAA 420

QY 421 CTCRAAAACCTAGAGGAGCTTCTCAAAAAGGAATCAGCCGTGTCGCTCCCAAAAAGAAAT 480
Db 421 CTCRAAAACCTAGAGGAGCTTCTCAAAAAGGAATCAGCCGTGTCGCTCCCAAAAAGAAAT 480

QY 481 GAGCTGTTAGTGGCAGAGATAGAGTATATGCAAGAGAGGGAATGGAGTTGCAACAAT 540
Db 481 GAGCTGTTAGTGGCAGAGATAGAGTATATGCAAGAGAGGGAATGGAGTTGCAACAAT 540

QY 541 AACATGATCTGCGAGCAAGATAGCCGAGGCGCCAGATTTGAATCCGAGCAGCAGGAA 600
Db 541 AACATGATCTGCGAGCAAGATAGCCGAGGCGCCAGATTTGAATCCGAGCAGCAGGAA 600

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Db 601 TCGAGTGTGATACAAAGGAGCAGCTTTACGAATCGGCTGATCTCTCATGACCACTCG 660

QY 661 CAGCAATTAATFCGGAATATATTCGGTGAACCTTCTTGAACCGGAATCAGCAATTCCTCC 720
Db 661 CAGCAATTAATFCGGAATATATTCGGTGAACCTTCTTGAACCGGAATCAGCAATTCCTCC 720

QY 721 GCCAAGACCAACCTCTCTCAACTGTTGTAACCTCAAAACATGATAACTGTTCTCTCC 780
Db 721 GCCAAGACCAACCTCTCTCAACTGTTGTAACCTCAAAACATGATAACTGTTCTCTCC 780

QY 781 CCTCATAAGATTAAGAGAGACGAGAGTTCATTTTATATTTTATAACGCGACTGTGT 840
Db 781 CCTCATAAGATTAAGAGAGACGAGAGTTCATTTTATATTTTATAACGCGACTGTGT 840

QY 841 ATTCATAGTTTAGGTTCTAATATGATAATAACAAACCTGTTCTTTGCTTCA 896
Db 841 ATTCATAGTTTAGGTTCTAATATGATAATAACAAACCTGTTCTTTGCTTCA 896


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RESULT 3
US-09-978-382A-3
; Sequence 3, Application US/09978382A
; Publication No. US2002019467A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-0009300S
; CURRENT APPLICATION NUMBER: US/09/978,382A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
US-09-978-382A-3

Query Match      100.0%; Score 896; DB 9; Length 896;
Best Local Similarity 100.0%; Pred. No. 3.5e-257;
Matches 896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCAATGGAGAGGTGGGAGTAGTCACGCGCAGAGAGTAGCAAGAACTAGGAGGA 60
Db 1 GGATCAATGGAGAGGTGGGAGTAGTCACGCGCAGAGAGTAGCAAGAACTAGGAGGA 60
Qy 61 GGGAAATAGATAGAGGATAGAGACACACAAACAACTGCTCAAGTTACTTTCTGCAAA 120
Db 61 GGGAAATAGATAGAGGATAGAGACACACAAACAACTGCTCAAGTTACTTTCTGCAAA 120
Qy 121 CGACCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATGCGGAAGTT 180
Db 121 CGACCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATGCGGAAGTT 180
Qy 181 GCCTCGTCACTCTCCACTCGTGGCGCTCTCTATGAGTACGCCACACACAGTGTGAGG 240
Db 181 GCCTCGTCACTCTCCACTCGTGGCGCTCTCTATGAGTACGCCACACACAGTGTGAGG 240
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Db 241 GGTACAATTTGAAAGGTACAGAAAGCTTGTTCGATGCCGTCAACCTCTCCGTCAACC 300
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Db 361 ATTCAAGATTTCAATAGGCATATTTGTTGGGAATCACTTGGTCTTGAACCTTCAAGGAA 420
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Db 421 CTCAAAAACCTAGAGGAGCTCTTTGAAAAGGAATCAGCCGTGTCCGCTCCAAAAAGAT 480
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Qy 541 AACATGTACCTCGGAGCAAGATAGCCGAGGCGCCAGGATTTGAATCCGGACACAGGAA 600
Db 541 AACATGTACCTCGGAGCAAGATAGCCGAGGCGCCAGGATTTGAATCCGGACACAGGAA 600
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Db 601 TCGAGTGTGATACAGGACGACAGCTTTACGAATCCGGTGTATCTTCTCATGACCAAGTCG 660
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Db 721 GGCAAGACCAACCTCTCTCAACTTGTGAACCTCAAAACATGATAACTTGTCTTCTTCC 780
Qy 781 CCTCATAACGATTAAAGAGAGAGAGAGTTCATTTTATATATAACGGAGCTGTGT 840
Db 781 CCTCATAACGATTAAAGAGAGAGAGAGTTCATTTTATATATAACGGAGCTGTGT 840
Qy 841 ATTCATAGTTTAGGTCTTAATAATGATATAACAACAACTGTTGTTCTTTCCTTCA 896
Db 841 ATTCATAGTTTAGGTCTTAATAATGATATAACAACAACTGTTGTTCTTTCCTTCA 896

RESULT 4
US-09-978-740A-3
; Sequence 3, Application US/09978740A
; Publication No. US20030005481A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-0009600S
; CURRENT APPLICATION NUMBER: US/09/978,740A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
US-09-978-740A-3

Query Match      100.0%; Score 896; DB 9; Length 896;
Best Local Similarity 100.0%; Pred. No. 3.5e-257;
Matches 896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCAATGGAGAGGTGGGAGTAGTCACGCGCAGAGAGTAGCAAGAACTAGGAGGA 60
Db 1 GGATCAATGGAGAGGTGGGAGTAGTCACGCGCAGAGAGTAGCAAGAACTAGGAGGA 60
Qy 61 GGGAAATAGATAGAGGATAGAGACACACAAACAACTGCTCAAGTTACTTTCTGCAAA 120
Db 61 GGGAAATAGATAGAGGATAGAGACACACAAACAACTGCTCAAGTTACTTTCTGCAAA 120
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Db 121 CGACCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATGCGGAAGTT 180
Qy 181 GCCTCGTCACTCTCCACTCGTGGCGCTCTCTATGAGTACGCCACACACAGTGTGAGG 240
Db 181 GCCTCGTCACTCTCCACTCGTGGCGCTCTCTATGAGTACGCCACACACAGTGTGAGG 240
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Db 361 ATTCAAGATTTCAATAGGCATATTTGTTGGGAATCACTTGGTCTTGAACCTTCAAGGAA 420
Qy 421 CTCAAAAACCTAGAGGAGCTCTTTGAAAAGGAATCAGCCGTGTCCGCTCCAAAAAGAT 480
Db 421 CTCAAAAACCTAGAGGAGCTCTTTGAAAAGGAATCAGCCGTGTCCGCTCCAAAAAGAT 480
Qy 481 GAGCTGTTAGTGCAGATAGATATATGCAGAGGAGGAATGGAATGCAACACAAT 540
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Qy 541 AACATGTACCTCGGAGCAAGATAGCCGAGGCGCCAGGATTTGAATCCGGACACAGGAA 600
Db 541 AACATGTACCTCGGAGCAAGATAGCCGAGGCGCCAGGATTTGAATCCGGACACAGGAA 600
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QY 541 AACATGTACCTGGAGCAAGATAGCCGAGGCGCCAGATTGAAATCCGGACCGCAGGAA 600
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Db 781 CCTCATAACGATTAAAGAGAGACGAGAGTTCATTTTATTTATTAACGGCACTGTGT 840
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RESULT 5
US-09-978-730-3
; Sequence 3, Application us/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE OF INVENTION: Plants
; FILE REFERENCE: 19452A-00092005
; CURRENT APPLICATION NUMBER: US/09/978,730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
US-09-978-730-3

Query Match 100.0%; Score 896; DB 10; Length 896;

Best Local Similarity 100.0%; Pred. No. 3.5e-257;
Matches 896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGATCAATGGAGGAGGTGGAGTAGTACAGGAGGAGAGAGTACGAAAGTACGAGGAG 60
Db 1 GGATCAATGGAGGAGGTGGAGTAGTACAGGAGGAGAGTACGAAAGTACGAGGAG 60
QY 61 GGGAAATAGACATAAAGAGGATAGAGAACACAAACAAATCGTCAAGTTACTTTCTGCAA 120
Db 61 GGGAAATAGACATAAAGAGGATAGAGAACACAAACAAATCGTCAAGTTACTTTCTGCAA 120
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Db 121 CGACGCAATGGTCTTCTCAAGAAAGCTTATGAATCTCTCTGTCTGTGTGTGATGCGGAAGTT 180
QY 181 GCCCTCGTCATCTTCTCCACTCGTGCCGCTCTATAGTACGCCACACACAGTGTGAGG 240
Db 181 GCCCTCGTCATCTTCTCCACTCGTGCCGCTCTATAGTACGCCACACACAGTGTGAGG 240
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QY 481 GAGCTGTAGTGGCAGAGATAGAGTATATGCAGAGAGGGAATGGAGTTGCAACACAAT 540
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QY 541 AACATGTACCTGGAGCAAGATAGCCGAGGCGCCAGATTGAAATCCGGACCGCAGGAA 600
Db 541 AACATGTACCTGGAGCAAGATAGCCGAGGCGCCAGATTGAAATCCGGACCGCAGGAA 600
QY 601 TCGAGTGTGATACAGGAGGAGCGAGATTAGCAATCCGGTGTATCTTCTCATGACCAATCGC 660
Db 601 TCGAGTGTGATACAGGAGGAGCGAGATTAGCAATCCGGTGTATCTTCTCATGACCAATCGC 660
QY 661 CAGCATTTAATCGGAATATATTCGGGTGAACCTCTTGAACCGAATCAGCAATTCCTCC 720
Db 661 CAGCATTTAATCGGAATATATTCGGGTGAACCTCTTGAACCGAATCAGCAATTCCTCC 720
QY 721 GGCAAGACCAACCTCTCTTCAACTGTGTGAACCTCAAAACATGATAACTGTTTCTTCTCC 780
Db 721 GGCAAGACCAACCTCTCTTCAACTGTGTGAACCTCAAAACATGATAACTGTTTCTTCTCC 780
QY 781 CCTCATAACGATTAAAGAGAGACGAGAGTTCATTTTATTTATTAACGGCACTGTGT 840
Db 781 CCTCATAACGATTAAAGAGAGACGAGAGTTCATTTTATTTATTAACGGCACTGTGT 840
QY 841 ATTACATAGTTTAGTTCTTAATTAATGATAATAACAAACTGTTGTTCTTCTTCTTCA 896
Db 841 ATTACATAGTTTAGTTCTTAATTAATGATAATAACAAACTGTTGTTCTTCTTCTTCA 896

RESULT 6
US-09-978-729A-5
; Sequence 5, Application us/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic

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; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978, 729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
; US-09-978-729A-5

Query Match          59.9%; Score 536.8; DB 9; Length 959;
Best Local Similarity 82.1%; Pred. No. 4.2e-150;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 6 AATGGAGGAAGTGGGAGTAGTCACGACGAGAGTAGCAAGAACTAGGGAGAGGGAA 65
Db 77 AATGGAGGTGGTGGCGATTAATGAAGTAGCAGAGCAGCAAGAGATAGGGAGGGAA 136
QY 66 AATAGAGATAAGAGATAGAGAACACACAAATCTCAAGTTACTTTCGCAACGAGC 125
Db 137 GATAGAGATAAGAGATAGAGAACACTACGAATCTCAAGTCACTTTCGCAACGAGC 196
QY 126 CAATGGTCTTCTCAAGAAAGCTTTATGAACCTCTCTGTGTGTGTGATGCCGAGTTGCCCT 185
Db 197 CAATGGTCTTCTCAAGAAAGCTTTATGAACCTCTCTGTGTGTGTGATGCCGAGTTGCCCT 256
QY 186 CGTCATCTTCTCCACCTCGTGGCGCTCTCTATGAGTAGCGCAACACAGTGTGAGGGGTAC 245
Db 257 TGTCTATCTTCTCCACCTCGAGGCGCTCTCTACGAGTAGCGCAACACAGTGTGAGAGAAC 316
QY 246 AATTGAAAGGTACAAGAAAGCTTTGTCGGATCGCGTCAACCCCTCTTCGTCACCGAAGC 305
Db 317 AATAGAAAGTACAAGAAAGCTTTGTCGGACGCGGTAAACCTCGACCATCACCGAAGC 376
QY 306 TAATCTACTAGTACTATCAGCAAGAACCTCTAAGCTTCGGAGGAGATTCGAGATATTCA 365
Db 377 TAATCTACTAGTACTATCAGCAAGAACCTCTAAGCTTCGGAGGAGATTCGAGGAGATTC 436
QY 366 GAATTCAAATAGCATATTGTTGGGAAATCAGTGGTTCCTTGAACCTCAAGGAACCTCA 425
Db 437 GAATTCGAACGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTAAAGGAACCTCA 496
QY 426 AAACCTAGAAGGACGCTTTGAAAGAAAGGAATCAGCGGTGTCGCGTCCCAAAAAGATGAGCT 485
Db 497 GAACCTTGAAGAGTAGGCTTGAGAAAGGAATCAGTCGTGTCGATCCGAAGACGAGAT 556
QY 486 GTTACTGGCAGAGATAGATATATGACAGAGAGGGAAATGGAGTTGCAACAATAAAT 545
Db 557 GTTACTGGCAGAGATTAATGATATGCAAAAAAGGAAATCGAGCTGCAAAACGATAAT 616

; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978, 729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
; US-09-978-729A-5

Query Match          59.9%; Score 536.8; DB 9; Length 959;
Best Local Similarity 82.1%; Pred. No. 4.2e-150;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 6 AATGGAGGAAGTGGGAGTAGTCACGACGAGAGTAGCAAGAACTAGGGAGAGGGAA 65
Db 77 AATGGAGGTGGTGGCGATTAATGAAGTAGCAGAGCAGCAAGAGATAGGGAGGGAA 136
QY 66 AATAGAGATAAGAGATAGAGAACACACAAATCTCAAGTTACTTTCGCAACGAGC 125
Db 137 GATAGAGATAAGAGATAGAGAACACTACGAATCTCAAGTCACTTTCGCAACGAGC 196
QY 126 CAATGGTCTTCTCAAGAAAGCTTTATGAACCTCTCTGTGTGTGTGATGCCGAGTTGCCCT 185
Db 197 CAATGGTCTTCTCAAGAAAGCTTTATGAACCTCTCTGTGTGTGTGATGCCGAGTTGCCCT 256
QY 186 CGTCATCTTCTCCACCTCGTGGCGCTCTCTATGAGTAGCGCAACACAGTGTGAGGGGTAC 245
Db 257 TGTCTATCTTCTCCACCTCGAGGCGCTCTCTACGAGTAGCGCAACACAGTGTGAGAGAAC 316
QY 246 AATTGAAAGGTACAAGAAAGCTTTGTCGGATCGCGTCAACCCCTCTTCGTCACCGAAGC 305
Db 317 AATAGAAAGTACAAGAAAGCTTTGTCGGACGCGGTAAACCTCCGACCATCACCGAAGC 376
QY 306 TAATCTACTAGTACTATCAGCAAGAACCTCTAAGTTTCGGAGGAGATTCGAGATATTCA 365
Db 377 TAATCTACTAGTACTATCAGCAAGAACCTCTAAGTTTCGGAGGAGATTCGAGGAGATTC 436
QY 366 GAATTCAAATAGGCATATTGTTGGGAAATCAGTGGTTCCTTGAACCTCAAGAACTCAA 425
Db 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTAAAGGAACCTCAA 496
QY 426 AAACCTAGAAGGACGCTTTGAAAGAAAGGAATCAGCGGTGTCGCGTCCCAAAAAGATGAGCT 485
Db 497 GAACCTTGAAGAGTAGGCTTGAGAAAGGAATCAGTGTGTCGATCCGAAGACGAGAT 556
QY 486 GTTACTGGCAGAGATAGATATATGCAAGAGAGGAAATGGAGTTGCAACAATAAAT 545
Db 557 GTTACTGGCAGAGATTAATGATATGCAAAAAAGGAAATCGAGCTGCAAAACGATAAT 616
QY 546 GTACCTCGGACGAAGATAGCGGAGGCGCCAGATTAATCGGACCAGCAGGAATCGAG 605
Db 617 GTATCTCCGCTCCAAAGATTACTGAA-----AGAACAGGTCTACAGCAACAAGATCGAG 670
QY 606 TGTGATACAAGGGACGACAGTTTACGAATCCGGTCTATCTTCTCATGACCAAGTCGAGCA 665
Db 671 TGTGATACATCAAGGGACAGTTTACGAGTCGGGTGTACTTCTTCTACAGATCGGGGCA 730
QY 666 TTATATCGGAATATATTCGGGTGAACCTTCTTGAACCGGAATACGCAATTTCTCCGGCCA 725
Db 731 GTATAACCGGAATATATTCGGGTGAACCTTCTTGAACCGGAATACGCAATTTCTCCCAACCA 790
QY 726 AGACCAACCTCCTTTCAACTTGTGTAACCTCAAAACATGATAACTTGT 775
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QY 546 GTACCTCGGACCAAGATAGCCGAAGGCGCAGATTGAATCCGGACCAAGGAGGATCGAG 605
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Db 617 GTATCTCCGTCCTCAAGATTACTGAA-----AGAACAGGTCTACAGCAACAAGAAATCGAG 670
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QY 606 TGTGATCAAGGACGACAGTTTACGAATCCGGTGTATCTCTCATGACCAAGTCCGACGA 665
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Db 671 TGTGATACATCAAGGACAGTTTACGAGTCGGGTGTACTTCTCTCACCAAGTCGGGCA 730
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QY 666 TTATATCGGAACATATATCCGGTGAACCTTCTTTGAACCGGAATCAGCAATTTCTCCGGGCA 725
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Db 731 GTATACCGGAATATATATGCGGTTAACTCTTTGAACCGGAATCAGAAATCTCTCCAACCA 790
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QY 726 AGACCAACCTCTCTTCAACTGTGTAACTCAAAACATGATAAATCTGTT 775
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Db 791 AGACCAACCACTCTGCAACTGTGTGATTGAGTCACTAACAATAAGCTTCTT 840
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RESULT 8
US-09-978-382a-5
; Sequence 5, Application US/09978382a
; Publication No. US20020194647A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000930US
; CURRENT APPLICATION NUMBER: US/09/978,382A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
US-09-978-382a-5

Query Match 59.9%; Score 536.8; DB 9; Length 959;
Best Local Similarity 82.1%; Pred. No. 4.2e-150;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 6 AATGGAGGAAGTGGGAGTAGTCACGACGACAGAGTAGCAAGAACTAGGGAGAGGGAA 65
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Db 77 AATGGAGGTTGGTCCAGTATGAAGTAGCAGAGCAGCAGAGAGATAGGGAGGGAA 136
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QY 66 AATAGAGATAAGAGGATAGAGAACACAACTCGTCAAGTTACTTTCTGCAACGACG 125
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Db 137 GATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAAGTCACCTTTCTGCAACGACG 196
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QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAATCTCTGTGTGTGATGCGCAAGTTGCCCT 185
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Db 197 CAATGGTCTTCTCAAGAAAGCTTATGAATCTCTGTGTGTGATGCGCAAGTTGCCCT 256
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QY 186 GGTATCTCTTCCACTCGTGGCGGTCTCTATGAGTACGCGCAACACAGTGTGAGGGGTAC 245
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Db 257 TGTATCTCTTCCACTCGAGCGGTCTCTACAGTACGCGCAACACAGTGTGAGAGGAAC 316
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QY 246 AATTGAAAGGTACAGAAGCTTTGTCGATGCCGTCAACCTCTTCCGTCAACCGAAGC 305
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Db 317 AATGAAAGGTACAGAAGCTTTGTCGATGCCGTCAACCTCTTCCGTCAACCGAAGC 376
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QY 306 TAATACTAGTACTATCAGCAAGAGCCCTCTAAGCTTCGAGGACGATTCGAGATATCA 365
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Db 377 TAATACTCAGTACTATCAGCAAGAGGCGTCTAAACTCCGGAGACAGATTCCGGACATTCA 436
QY 366 GAATTCAAATAGCATATTTGGGGAATCAGCTTGGTTCCTTGAACCTTCAAGGAACCAA 425
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Db 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTGAAGGACCTCAA 496
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QY 426 AAACCTTAGAAGGACGCTCTTGAAGAAAGGAATCAGCCGTGTCCGCTCCAAAAGAAATAGCT 485
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Db 497 GAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCCGATCCCAAGAACGACGAGAT 556
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QY 486 GTTAGTGGCAGAGATAGATATATGAGAAAGAGGAAATGAGTGTGCAACACATATACAT 545
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Db 557 GTTAGTTGCAGAGATTGAATACATGCAAAAAGGGAATCAGCTGCAAAAACGATAACAT 616
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QY 546 GTACCTGCGAGCAAGATAGCCGAAGGCGCAGATTGAATCCGGACCAAGGAAATCGAG 605
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Db 617 GTATCTCCGCTCCAAGATTACTGAA-----AGAACAGGTCTACAGCAACAAGAAATCGAG 670
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QY 606 TGTGATACAAAGGACGACAGTTTACGAATCCGGTGTATCTCTCATGACCAAGTCCGACGA 665
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QY 666 TTATATCGGAACATATATCCGGTGAACCTTCTTTGAACCGGAATCAGCAATTTCTCCGGGCA 725
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QY 726 AGACCAACCTCTCTTCAACTGTGTAACTCAAAACATGATAAATCTGTT 775
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Db 791 AGACCAACCACTCTGCAACTGTGTGATTGAGTCACTAACAATAAGCTTCTT 840
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RESULT 9
US-09-978-740a-5
; Sequence 5, Application US/09978740a
; Publication No. US20030005481A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000960US
; CURRENT APPLICATION NUMBER: US/09/978,740A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
US-09-978-740a-5

Query Match 59.9%; Score 536.8; DB 9; Length 959;
Best Local Similarity 82.1%; Pred. No. 4.2e-150;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 6 AATGGAGGAAGTGGGAGTAGTCACGACGACAGAGTAGCAAGAACTAGGGAGAGGGAA 65
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 AATGGAGGTTGGTCCAGTATGAAGTAGCAGAGCAGCAGAGAGATAGGGAGGGAA 136
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 66 AATAGAGATAAGAGGATAGAGAACACAACTCGTCAAGTTACTTTCTGCAACGACG 125
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Db 137 GATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAAGTCACCTTTCTGCAACGACG 196
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QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAATCTCTGTGTGTGATGCGCAAGTTGCCCT 185
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Db 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTGTGTGACGCTGAGGTTGCTCT 256
QY 186 CGTCATCTTCTCCACTCGTGGCCGCTCTATGAGTACGCCAACACAGTGTGAGGGGTAC 245
Db 257 TGTGATCTTCTCCACTCGAGCCGCTCTACGAGTACGCCAACACAGTGTGAGAGGAAC 316
QY 246 AATTGAAAGTCAAGAAAGCTTGTTCGATCGCGTCAACCCCTCCGTCACCGAAGC 305
Db 317 AATAGAAAGGTACAAGAAAGCTTCTCCGACGCGTAAACCTCCGACCATCACCGAAGC 376
QY 306 TAATCTCAGTACTATCAGCAAGAGCCTCTAAGCTTCGGAGGCGAGTTCGAGATATTCA 365
Db 377 TAATCTCAGTACTATCAGCAAGAGGCGTCTAACTCCGAGACAGATTCGGGACATTCA 436
QY 366 GAATTCAAATAGGATATTGTTGGGAACTCACTTGGTTCCTTGAACCTTCAAGGAAGTCAA 425
Db 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTAAAGAACTCAA 496
QY 426 AAACCTAGAGGAGCTTCTGAAAGAAATCAGCGGTCGCGTCCCAAAAAGAAATGAGCT 485
Db 497 GAACCTTGAAGCTAGGCTTCTGAGAAAGAAATCAGTCTGTCGATCCCAAGAAAGCAGAGAT 556
QY 486 GTTAGTGCAGAGATAGATATATGAGACAGAGGAAATGAGCTTGCACACAAATAACAT 545
Db 557 GTTAGTGCAGAGATTAATATACATGCAAAAGGAAATGAGCTGCAAAAGCAATAACAT 616
QY 546 GTACCTGCGAGCAAGATAGCCGAAGCGCAGATTTGAATCCGACACAGGAGATCGAG 605
Db 617 GTATCTCCGCTCCAAGATTAAGTCA-----AGAACAGGCTCTACAGCAACAGATCGAG 670
QY 606 TGTGATACAGGACACAGATTTACGAATCCGGTGTATCTCTCATGACCGAGTCCGACGA 665
Db 671 TGTGATACATCAAGGACAGTTTACGAGTCCGGTGTACTTCTCTCACCAGTCGGGCA 730
QY 666 TTATAATCGGAATATATTCGCGTGAACCTTCTTGAACCAATCAGCAATTCCTCGGCA 725
Db 731 GTATAACCGGAATTAATTCGCGTTAACTTCTTGAACCAATCAGCAATTCCTCAACCA 790
QY 726 AGACCAACCTCTCTTCAACTTGTGAATCTCAAAACATGATACTTGT 775
Db 791 AGACCAACCACTCTGCAACTTGTGATTCAGTCTAACATAAGCTTCT 840

RESULT 10
US-09-978-730-5
; Sequence 5, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE OF INVENTION: Plants
; FILE REFERENCE: 19452A-00092005
; CURRENT APPLICATION NUMBER: US/09/978,730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
US-09-978-730-5

Query Match 59.9%; Score 536.8; DB 10; Length 959;
Best Local Similarity 82.1%; Pred. No. 4.2e-150;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;
QY 6 AATGGAGGAAGTGGGAGTAGTCAGACGACGAGAGTAGCAAGAAATAGGAGAGGGAA 65
Db 77 AATGGAGGTGGTGGAGTAGTAAGTAGACGAGACGACGAGAGATAGGAGAGGGAA 136
QY 66 AATAGAGATAAGAGGATAGAGAACACAAATCTCAGTTACTTCTTGCACCAAGC 125
Db 137 GATAGAGATAAGAGGATAGAGAACACTACGAATCTGATGATGCCAAGTTGCTCT 185
QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAATCTCTGCTGTGTGATGCCAAGTTGCTCT 256
Db 197 CAATGGTTACTCAAGAAAGCTTATGAGCTCTCTGCTGTGTGAGCTCAGGTTGCTCT 256
QY 186 CGTCATCTTCTCCACTCGTGGCCGCTCTATGAGTACGCCAACACAGTGTGAGGGTAC 245
Db 257 TGTGATCTTCTCCACTCGAGGCGCTCTACGAGTACGCCAACACAGTGTGAGAGGAAC 316
QY 246 AATTGAAAGGTACAGAAAGCTTGTTCGATCGCGTCAACCCCTCTTCCGACCGAAGC 305
Db 317 AATAGAAAGGTACAGAAAGCTTGTCTCCGACGCGTAAACCTCCGACCATCACCGAAGC 376
QY 306 TAATCTCAGTACTATCAGCAAGAGCCTCTAAGCTTTCGGAGGCGAGATTCGAGATATTCA 365
Db 377 TAATCTCAGTACTATCAGCAAGAGGCGTCTAACTCCGAGACAGATTCGGGACATTCA 436
QY 366 GAATTCAAATAGGATATTGTTGGGAAATCACTTGGTTCCTTGAACCTTCAAGGAAGTCAA 425
Db 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTAAAGGAAGTCAA 496
QY 426 AAACCTAGAGGAGCTTCTGAAAGAAATCAGCGGTCGCGTCCCAAAAAGAAATGAGCT 485
Db 497 GAACCTTGAAGTAGGCTTGTGAAAGAAATCAGTCTGTCGATCCCAAGAAAGCAGAGAT 556
QY 486 GTTAGTGCAGAGATAGATATATGAGAGAGGAAATGAGTTGAATCCGGACCGAGAAATCGAG 605
Db 557 GTTAGTGCAGAGATTAATATACATGCAAAAGGAAATCGAGTGCACAAACGATTAACAT 616
QY 546 GTACCTGCGAGCAAGATAGCCGAAGGCGCAGATTTGAATCCGGACCGAGAGAAATCGAG 670
Db 617 GTATCTCCGCTCCAAGATTAAGTCA-----AGAACAGGCTCTACAGCAACAGATCGAG 670
QY 606 TGTGATACAGGAGGACGAGATTTACGAATCCGGTGTATCTCTCATGACCGAGTCCGACGA 665
Db 671 TGTGATACATCAAGGACAGTTTACGAGTCCGGTGTACTTCTCTCACCAGTCGGGCA 730
QY 666 TTATAATCGGAATATATTCGCGTGAACCTTCTTGAACCAATCAGCAATTCCTCGGCA 725
Db 731 GTATAACCGGAATTAATTCGCGTTAACTTCTTGAACCAATCAGCAATTCCTCAACCA 790
QY 726 AGACCAACCTCTCTTCAACTTGTGAATCTCAAAACATGATACTTGT 775
Db 791 AGACCAACCACTCTGCAACTTGTGATTCAGTCTAACATAAGCTTCT 840

RESULT 11
US-09-770-445-644/C
; Sequence 644, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.

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; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Huzban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770.445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 644
; LENGTH: 845
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-770-445-644

Query Match          21.9%; Score 196.2; DB 10; Length 845;
Best Local Similarity 66.4%; Pred. No. 1.3e-48;
Matches 282; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 176 AAGTTGCCCTCGTCATCTTCCCACTCGTGGCCGCTCTATCAGTACGCCCAACAACAGT 235
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 845 AAGTTGCCCTATTTCTTCTCCACTCGTGGCCGCTCTATGAATACGCCCAATAACAACA 786
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 236 TCAGGGGTACRAATTCGAAGGTACAAGAGTGTGTTCCGATCGCGTCAACCCCTCCCTCCG 295
Db      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 785 TAAGATCAACCAATGAGAGGTACAAGAGCTGTGTTCTGATAGCCCAACACTAGCACTG 726
Db      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 296 TCACCGAAGCTAATACTCAGTACTATCAGCAAGAAGCCCTTAAGCTTCGGAGGCAGATTC 355
Db      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 725 TCCAAGAAATCAATCCCGGTACTATCAACAAGAATCTGTAAGCTGAGACACAGATCC 666
Db      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 356 GAGATATTCAGNAATTCARAATAGGCATATTGTTGGGAATCACTTGCTTCTTGAACCTCA 415
Db      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 665 AAACGATCAAAACTCCCAACAGGAATCTCATGGGAGACHTTTTGAGTTCTCTTAAGTGTC 606
Db      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 416 AGGAACCTCAAAACCTAGAGGACGCTTTGAAAAAGGAATCAGCCGTGCGCTCCAAAA 475
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 605 AGGAACAAAAACAAGTTGAGATCGCCTTGAGAAAGCTATCTTAGGATCAGGTCCAAAGA 546
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 476 AGAATGAGCTGTAGTGGCAGAGATAGATATATGAGAGAGGGAATGGAGTTGCAAC 535
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 545 AGCATGAGTTGCTTTTAGTTGAAATCGAAAACGCCGAGAAAAGGGAGATTGAGCTTGACA 486
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 536 ACAATAACATGTACCTCGCAGCAAAAGATAGCCGAGCGCCAGATTGAATCCGAGCAGC 595
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 485 ATGAGAACATCTATCTAAGAACTAAGTAGCAGAGAGTGGAGAGGTATCAACAACCATC 426
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 596 AGGAA 600
Db      |||
Qy 425 ATCAA 421
Db      |||

RESULT 12
US-09-938-842A-1776
; Sequence 1776, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
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; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1776
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1776

Query Match          18.6%; Score 166.6; DB 9; Length 645;
Best Local Similarity 58.0%; Pred. No. 7.5e-40;
Matches 295; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

Qy 53 TAGGGAGAGGGAAATAAGAGATAAAGAGGATAGAGACACACAACAATCGTCAAGTTACTT 112
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 113 TCTGCAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTCTTGTGTGATG 172
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 62 TCTCCAAAAGAAAGGATGGTGTGTTGAAGAAAGCCTTTGAGCTCTCAGTGTCTTGTGATG 121
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 173 CCGAAGTTGCCCTCGTCATCTTCTCCACTCGTGGCCGCTCTCTATGATGACGCCAACACA 232
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 122 CTGAGTTTCTCTTATCATCTTCTCTCTAAAGCAAACTTTATGAATTCGCCAGCTCCA 181
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 233 GTGTGAGGGGTACAAATGAAAGGTACAAAGGCTTGTTCGATGCCCTCAACCCCTCTT 292
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 182 ATATGCAAGATACCATAGATCGTTTATCTGAGGCATCTACTAAGGATCGATCAGCACCAAC 241
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 293 CCGTCACCGAAGCTAATACTCAGTACTATCAGCAAGAGCCTCTAAGCTTCGGAGGCGAGA 352
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 242 CGGTTCTGGAAGAAATATGCGCATTTTGAATATGAAGCAACAACATGATGAAGAAA 301
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 353 TTCGAGATATTTCAGAAATCAAAATAGGCATATGTTGGGGAATCACTTGGTTCCTTGAAC 412
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 302 TTGAACAACCTCGAAGCTTCTAAAGCTAAACTCTTGGGAGAGGCATAGGAACATGCTCAA 361
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 413 TCAGGAGACTCAAAAACCTAGAAGACGCTTTGAAAAAGGAATCAGCCGTGTCGCTCCA 472
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 362 TCGAGGAGCTCCACAGATTGAGCAACAGCTTGAGAAAAGTCTCAATGCTATTCGAGCAA 421
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 473 AAAAGAATGAGCTGTAGTGGCAGAGATAGAGTATATGCAAGAAGGGAATGGAGTTCC 532
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 422 GAAAGACTCAAGTGTGTTAAGGAACAAATTGAGCAGCTCAAGCAAAAGGAGAAAGCTCTAG 481
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 533 AACACAATAACATGTACCTCGCAGCAAG 561
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 482 CTGCAGAAAACGAGAAGCTCTCTGAAAAG 510
Db      ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-853-450-33
; Sequence 33, Application US/09853450
; Publication No. US2002019465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Gary
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: Exhibiting Modulated Reproductive Development
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 33
; LENGTH: 645
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(645)
; OTHER INFORMATION: AGL20 (SUPPRESSOR OF CONSTANS (CO) OVEREXPRESSION
US-09-853-450-33

Query Match      18.6%; Score 166.6; DB 9; Length 645;
Best Local Similarity 58.0%; Pred. No. 7.5e-40;
Matches 295; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 53 TAGGAGAGGGAATAAGAGGATAGAGATACAGACACAAACAAATCGTCAAGTTACTT 112
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Db 2 TGGTAGGGGCAAACTCAGATGAAGAGATAGAGATGCAACAAGCAGACAACTGACTT 61
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QY 113 TCTGCAACGACGCAATGGCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATG 172
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 TCTCAAAAGAGGAATGGTTTGTGAAGAAAGCCTTTGAGCTCTCAGTCTTGTGTGATG 121
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 173 CGAAGTTGCCCTCGCTCATCTTCTCCACTCGTGGCGCTCTATGATGACGCCAACAA 232
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 CTGAAGTTTCTTATCAFTTCTCTCTCAAAGGCAAACTTTTATGAATTCGCCAGCTCCA 181
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QY 233 GTGTGAGGGGTACAATTTGAAGGTACAAGAGCTTGTTCGGATGCGTCAACGCTCCTT 292
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Db 182 ATATGCAAGATACCATAGATCGTTATCTGAGGCATCTATGAGTTCAGTCAAGCACAAC 241
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QY 293 CCGTCACCGAAGCTAATCTAGTACTATCAGCAAGAAAGCCTCTAAGCTTCGGAGGCAGA 352
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 242 CGGTTTCTGAAGAAATATGCAAGCATTTCAAAATATCAAGCAGCAACATGATGAAGAAA 301
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QY 353 TTCGAGATATTCAGAACTCAATAGGCATATTGTTGGGGAATCACTTGTTCCTTGAAC 412
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Db 302 TTGAACAACTCGAGCTTCTAAAGTAACTCTTGGGAAAGGCATAGGAACATGCTCAA 361
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QY 413 TCAAGGAACTCAAAACCTAGAAAGACGCTTTGAAAGGAATCAGCGGTGTCGGCTCCA 472
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Db 362 TCGAGGAGCTCAACAGATTTGAGCAACAGCTTGAGAAAGTGTCAATGTATTCGAGCAA 421
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QY 473 AAAGAATGACTGTTAGTGGCAGAGATAGATATATGATGAGAGAGGGAATGGAGTTGC 532
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 GAAAGACTCAAGTGTGTTAAGGAACAAATTTGACAGCTCAAGCAAAAGGAGAAAGCTTAG 481
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 533 AACACAATACTGTACCTGCGAGCAAG 561
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 CTGCAAGAACGAGAGCTCTCTGAAAG 510
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RESULT 14
US-09-978-729a-1
; Sequence 1, Application US/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978,729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-729a-1

Query Match      16.7%; Score 149.2; DB 9; Length 1062;
Best Local Similarity 57.0%; Pred. No. 1.5e-34;
Matches 293; Conservative 0; Mismatches 218; Indels 3; Gaps 1;

QY 53 TAGGAGAGGGAATAAGAGATAGAGATTAAGAGATAGACACACAAACAAATCTCTCAAGTTACTT 112
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Db 102 TGGGAAGAGTAGGGTTTCAGCTGAAGAGATAGAGACAAAGATCAATAGGCAAGTTACTT 161
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QY 113 TCTGCAAAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATG 172
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Db 162 TCTCAAAAGAGAAGTCTGGTTGCTCAAGAAAGCTCATGAGATCTGTCTCTCGGATG 221
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 173 CGAAGTTGCCCTCGCTCATCTTCTCCACTCGTGGCGCTCTATGATGACGCCAACAAAC - 231
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Db 222 CTGAGTTGCTCTCATCTCTTCTTCCAAAGGCAAACTCTTCGAATATTCACCGACT 281
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QY 232 --AGTGTGAGGGGTACAATTTGAAGGTACAAGAGCTTGTTCGGATGCCGTCAACCCCTC 289
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Db 282 CTGCAATGAGAGATCTTGAACGCTATGATCGCTATTATTCAGACAAACAACTTG 341
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QY 290 CTTCCTCACCGAAGCTTAATCTCAGTACTATCAGCAAGAGCCCTCTAAGCTTCGGAGGC 349
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Db 342 TTGGCGGAGACGTTTCACAAAGTGAATTTGGGTTCTAGAACATGCTAAGCTCAAGGCAA 401
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QY 350 AGATTTCGAGATATTCAGAAATCAATAGGCAATATTTGGGGAATCACTTGGTTCCTTGA 409
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Db 402 GAGTTGAGTACTTTGAGAGAACAAAGAAATTTATGGGGGAAGATCTTGATTGCTTGA 461
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QY 410 ACTTCAAGGAACCTCAAAACCTTAGAAGGAGCTCTTTGAAAAGAGGATCAGCGTGTCCGCT 469
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 462 GCTTGAAGAGCTTCCAAAGCTTTGGAGCATCAGCTCGATGAGCTATCAGAGCATTAGGT 521
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QY 470 CCAAAAGAAATGAGCTGTTAGTGGCAGAGATAGATATATCAGAAAGAGGAAATGGAGT 529
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Db 522 CAAGAAGAACCAAGCTATGTTGCAATCCATATCTGCGCTCCAGAAGAGGATAAAGCT 581
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QY 530 TGCACACAAATACATGTACCTGCGAGCAAGAT 563
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Db 582 TCGAGATCACAAATTCGCTTCTCAAAAAGAT 615
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RESULT 15
US-09-981-087A-1
; Sequence 1, Application US/09981087A
; Patent No. US20020178466A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: Farrandiz, Cristina
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000940US
; CURRENT APPLICATION NUMBER: US/09/981,087A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-981-087A-1

Query Match      16.7%; Score 149.2; DB 9; Length 1062;
Best Local Similarity 57.0%; Pred. No. 1.5e-34;
Matches 293; Conservative 0; Mismatches 218; Indels 3; Gaps 1;

QY 53 TAGGGAGAGGGAATAAGAGGATAGAGACACAAACAAATCGTCAAGTTACTT 112
Db 102 TGGGAAGAGGTAGGGTTACGCTGAAGAGGATAGAGACAGATCAATAGGCAAGTTACTT 161
QY 113 TCTCCAACGACGCAATGGCTTCTCAAGAAAGCTTATGAACCTCTCTCTTGTGTGATG 172
Db 162 TCTCAAGAGAAAGCTCTGGTTTGTCAAGAAAGCTCATGAGATCTCTCTCTCGGATG 221
QY 173 CCGAAGTTGCCTCGTCTATCTTCCACTCTGCGCGTCTCTATGAGTACGCCAACAAAC - 231
Db 222 CTGAGGTTGCTCTCATCGTCTCTCTTCCAAAGGCMAACTCTTCGAATATCCACCGACT 281
QY 232 --AGTGTGAGGGTACAAATTGAAAGGTACAAGAAAGCTTGTTCGGATGCCGTCAACCCTC 289
Db 282 CTTGCATGGAGAGGATACCTTGACGCTATGATCGCTATTATATTCAGACAAACAACCTTG 341
QY 290 CTTCCGTCACCGAAGCTAATACTCAGTACTATATCAGCAAGAAGCCCTTAAGCTTCGGAGGC 349
Db 342 TTGCCCGAGAGGTTTCACAAAGTGAAATTTGGGTCTTAGACATGCTTAGCTCAAGGCCAA 401
QY 350 AGATTTCGAGATATTTCAGAAATTCAAATAGGCAATATGTTGGGGAATCACTTGGTTCTTTGA 409
Db 402 GAGTTGAGGTACTTGAGAGAAACAAAGGAATTTATGGGGAAGATCTTGATTCGTTGA 461
QY 410 ACTTCAAGGAACTCAAAACCTAGNAGGACGCTCTGAAAAGGAATCAGCCGTGTCGCCGT 469
Db 462 GCTTGAAGGAGCTCCAAAGCTTGGAGCATCAGCTCGATGCAGCTATCAGAGCATTAGGT 521
QY 470 CCAAAAAGAATGAGCTGTTAGTGGCAGAGATAGATATATGCAAGAGGGGAAATGGAGT 529
Db 522 CAAGNAGAACCAAGCTATGTTCCGAATCCATATCTGCGCTCCAGAGAGGAGATAAAGCCT 581
QY 530 TGCAACACAATAACATGTACCTGGCAGCAAGAT 563
Db 582 TGCAAGATCACAACAATTCGCTTCTCAAAAAGAT 615
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Job time : 56.234 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 05:45:28 ; Search time 221.706 Seconds

(without alignments)

9101.213 Million cell updates/sec

Title: US-09-978-382a-3

Perfect score: 896

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	887	99.0	1202	21	AAV99859
3	536.8	59.9	959	20	AAV99860
4	532.4	59.4	777	21	AAV99860
5	335.8	37.5	5622	20	AAV99857
6	335.8	37.5	5622	24	AAH77274
7	326.6	36.5	1143	17	AAH77274
8	322	35.9	511	21	AAV99857
9	312.6	34.9	714	22	AAV99857

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13	311.6	34.8	511	21	ABK43357	Arabidopsis thalia
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15	305.2	34.1	1201	21	AAF57947	Poplar floral home
16	305.2	34.1	1219	22	AAF85398	Nucleotide sequenc
17	305.2	34.1	1219	22	ABK88489	Poplar floral home
18	290.8	32.5	1157	21	AAZ50201	Petunia hybrida ne
19	290.8	32.5	1157	21	AAZ35494	Petunia nectary-sp
20	282.4	31.5	1053	21	AAZ43362	Arabidopsis thalia
21	282.4	31.5	1053	21	AAZ43362	Arabidopsis thalia
22	274.2	30.6	903	21	AAZ37453	Arabidopsis thalia
23	269.4	30.1	997	17	AAZ34432	Eucalyptus AGE2 cd
24	259.6	29.0	706	21	AAZ55965	Eucalyptus grandis
25	252.6	28.2	1218	21	AAZ43678	zea mays DNA fragm
26	248.2	27.7	805	24	ABK82084	DNA encoding novel
27	248.2	27.7	1259	24	ABK82131	DNA encoding novel
28	245	27.3	909	21	AAV99364	Plant PRAGI promot
29	231.8	25.9	581	21	AAZ57270	Eucalyptus grandis
30	219	24.4	1321	21	AAZ47718	zea mays DNA fragm
31	196.2	21.9	845	24	ABN98876	Arabidopsis thalia
32	188	21.0	6138	20	AAV99858	Arabidopsis AG15 g
33	188	21.0	6138	24	AAH77275	Arabidopsis dehisc
34	177	19.8	466	21	AAZ35890	zea mays DNA fragm
35	166.6	18.6	1075	21	AAZ43663	Arabidopsis thalia
36	159	17.7	498	20	AAV69758	Tobacco ovary-spec
37	158	17.6	1144	19	AAV18014	Pinus radiata cone
38	157.6	17.6	352	21	AAZ55878	Eucalyptus grandis
39	155	17.3	423	21	AAZ56741	Eucalyptus grandis
40	154.2	17.2	457	21	AAZ41474	zea mays DNA fragm
41	153	17.1	1075	21	AAZ37803	Arabidopsis thalia
42	149.2	16.7	1062	20	AAZ18594	Arabidopsis AG18 n
43	149.2	16.7	1062	20	AAV99856	Arabidopsis AG18-1
44	147.6	16.5	1123	21	AAZ41877	Arabidopsis thalia
45	143.2	16.0	1342	18	AAZ99437	Maize floral meris

ALIGNMENTS

RESULT 1
AAV99859
ID AAV99859 standard; cDNA; 896 BP.
XX AAV99859;
AC AAV99859;
XX
DT 10-MAY-1999 (first entry)
XX
DE Arabidopsis AGL1 cDNA.
XX
KW AGL1-like gene; agamous-like 1 gene; seed dispersal; dehiscence;
KW transgenic plant; promoter; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 7..753
FT /*tag= a
FT polyA_site 896
FT /*tag= b
XX
PN WO9900502-A1.
XX
PD 07-JAN-1999.
XX
PF 25-JUN-1998; 98WO-US13208.
XX
PR 28-APR-1998; 98US-0067800.
XX
PR 27-JUN-1997; 97US-0051030.
XX
PA (REGC) UNIV CALIFORNIA.

PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
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PR 26-OCT-1999; 99US-0161361.

RESULT 3
AAV99860
ID AAV99860 standard; cDNA: 959 BP.

[illegible]

RESULT 3
AAV99860
ID AAV

Db	257	TGTCATCTTCTCCACTCGAGCCCTCTCTACGAGTACGCCAACACAGTGTGAGAGAAC	316
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Db	317	AATAGAAAGGTACAAGAAGCTTCTCGACGCCGTTAACCCCTCGACCCATCACCGAAGC	376
QY	306	TAACTCAGTACTATCAGCAAGAAGCCTCTAAGCTTCGGAGGAGATTTCGAGATAATTCA	365
Db	377	TAACTCAGTACTATCAGCAAGAAGGCGTCTAAACTCCGGAGACAGATTTCGGACATTCA	436
QY	366	GAATTCAAAATAGGCATATTTGCGGGAATCACTTGGTTCCTTGAACCTTCAAGGAACCTCA	425
Db	437	GAATTTGACAGACACATTTCTTGTGAATCTCTTGGTTCCTTGAACCTTAAAGGAACCTCA	496
QY	426	AAACCTAGAAGGACGCTTTGAAAAAGGAATCAGCGGTGTCGCTCCAAAAAGAAATGAGCT	485
Db	497	GAACCTTGAAAGTAGGCTTCAGAAAGGAATCAGTCGTCGATCCAGAAGACCGAGAT	556
QY	486	GTTAGTGGCAGACATAGAGTATATGCAGAGAGGGAATGGAGTTGCAACAATAACAT	545
Db	557	GTTAGTGCAGAGATTGAATACATGCAAAAAGGGAATCAGCTGCAAAACGATAACAT	616
QY	546	GTACCTCGCAGCAAGATAGCCGAAGCGCCAGATTGAATCCGACACAGCAGGAATCCAG	605
Db	617	GTATCTCCGCTCCAAGATTACTGAA-----AGAACAGGCTACAGCAACAAGAAATCCAG	670
QY	606	TGTGATACAAGGACACACAGTTTACGAATCCGGTGTATCTTCTCATGACCAATGCGCAGCA	665
Db	671	TGTGATACATCAAGGACACAGTTTACGAGTCGGGTGTACTTCTTCTCACCAGTCGGGSCA	730
QY	666	TTATATTCGGAACATATATCCGGTGAACCTTCTTGAACCGAAATCAGCAATTCTCCGGCCA	725
Db	731	GTATACCGGAATTATATTCGGGTAACTTCTTGAACCGAAATCAGAAATTCCTCCAAGCA	790
QY	726	AGACCAACCTCTCTTCAACTTGTGAATCTCAAAACATGATACTTCTTT	775
Db	791	AGACCAACCACTCTGCAACTTGTGATTCACTTCAACATAAGCTTCTT	840
RESULT 4			
AAC43464			
ID	AAC43464 standard; DNA; 777 BP.		
AC	AAC43464;		
XX			
DT	17-OCT-2000 (first entry)		
XX			
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 39336.		
XX			
KW	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway;		
XX	metabolic pathway; promoter; termination sequence; ss.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EPI033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-0301439.		
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PR	25-FEB-1999; 99US-0121825.		
PR	05-MAR-1999; 99US-0123180.		
PR	09-MAR-1999; 99US-0123548.		
PR	23-MAR-1999; 99US-0125788.		
PR	25-MAR-1999; 99US-0126264.		
PR	29-MAR-1999; 99US-0126785.		
PR	01-APR-1999; 99US-0127462.		
PR	06-APR-1999; 99US-0128234.		
PR	08-APR-1999; 99US-0128714.		
PR	16-APR-1999; 99US-0129845.		
PR	19-APR-1999; 99US-0130077.		


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Db 655 TATAACCGGAATTATATGCGGTAACTTCTTGAACCGAATCAGAATTCCTCCAAACAA 714
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Db 715 GACCAACCACTCTGCAACTTAGGACCTAATAATTTACATATATCTTGATT 766

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ID AAV99857 standard; cDNA; 5622 BP.
XX AAV99857;
AC AAV99857;
XX
DT 10-MAY-1999 (first entry)
XX
DE Arabidopsis AGL1 gene.
XX
KW AGL1-like gene; agamous-like 1 gene; seed dispersal; dehiscence;
KW transgenic plant; promoter; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key
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FT /*note= "contains introns"
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FT 1606..2832
FT /*tag= b
FT intron
FT 2833..4128
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FT /*note= "this region is specifically claimed in
FT Claim 26 as a dehiscence zone-selective
FT regulatory element"
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FT intron
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FT Claim 26 as a dehiscence zone-selective
FT regulatory element"
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FT intron
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FT /*tag= g
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FT Claim 26 as a dehiscence zone-selective,
FT regulatory element"
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FT Claim 26 as a dehiscence zone-selective
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FT Claim 26 as a dehiscence zone-selective
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FT exon
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FT Claim 26 as a dehiscence zone-selective
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XX 07-JAN-1999.
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XX 25-JUN-1998; 98WO-US13208.
PF
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PR 28-APR-1998; 98US-0067800.
PR 27-JUN-1997; 97US-0051030.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Ferrandiz C, Yanofsky MF;
PI
XX WPI; 1999-095747/08.
DR P-PSDB; AAW80999.
XX
XX Use of agamous-like nucleic acids - useful for the production of
XX transgenic seed plants in which dehiscence is modified resulting in
XX delayed seed dispersal
XX
XX Claim 12; Fig 7; 126pp; English.
XX
XX This is the nucleotide sequence of the Arabidopsis agamous-like 1
XX (AGL1)-like gene, including the promoter region and coding exons
XX (see also AAW80999). The invention provides a transgenic seed plant,
XX such as an agl1 and agl5 double mutant, that is characterised by
XX delayed seed dispersal due to suppression of AGL1 and AGL5 (see
XX AAV99858) expression. The invention also provides dehiscence zone
XX regulatory elements, derived from the AGL1 or AGL5 gene, that
XX confer selective expression upon an operatively linked nucleic
XX acid molecule in the valve margin or dehiscence zone of a seed
XX plant. The transgenic seed plants include members of the
XX Brassicaceae, such as rapeseed, and members of the fabaceae, such
XX as soybean, pea, lentil and bean. A plant expression vector
XX comprising a dehiscence zone-selective regulatory element, and a
XX kit for producing the transgenic seed plants are also provided.
XX
XX Sequence 5622 BP; 1854 A; 929 C; 906 G; 1926 T; 7 other;
SQ

Query Match 37.5%; Score 335.8; DB 20; Length 5622;
Best Local Similarity 99.4%; Pred. No. 2.8e-92;
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 558 AAAGATAGCCGGAAGCGCCAGATTGAATCCGACACGAGGAATCGAGTGTGATACAGG 617
Db 5025 ATAGATAGCCGGAAGCGCCAGATTGAATCCGACACGAGGAATCGAGTGTGATACAGG 5084
QY 618 GACGACAGTTTACGAATCGGGTGTATCTTCTATGACCATCGCAGCATTTATATCGGAA 677
Db 5085 GACGACAGTTTACGAATCGGGTGTATCTTCTATGACCATCGCAGCATTTATATCGGAA 5144
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QY	678	CTATATTCGGGTGAACCTTCTTGAACCGAATCAGCAATTCCTCGGGCCAAAGCAACCTCC	737
Db	5145	CTATATTCGGGTGAACCTTCTTGAACCGAATCAGCAATTCCTCGGGCCAAAGCAACCTCC	5204
QY	738	TCTTCAACTTGTGTAACCTCAAAACATGATAACTTGTCTTCCCTCATACAGATTAA	797
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QY	798	GAGACGAGAGAGTTCATTTATTTATAACCGCGACTGTGTATTCATAGTTAGGTTTC	857
Db	5265	GAGACGAGAGAGTTCATTTATTTATAACCGCGACTGTGTATTCATAGTTAGGTTTC	5324
QY	858	TAATAATGATAATAACAAACTGTCTTCTTCTTCTTCA	896
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RESULT 6			
AAH77274	ID AAH77274 standard; DNA; 5622 BP.		
XX	AC	AAH77274;	
XX	DT	06-FEB-2002 (first entry)	
XX	DE	Arabidopsis dehiscence zone-selective SHP1 regulatory element.	
XX	KW	IND1; indehiscent 1; fruit dehiscence; oil seed rape; SHP1;	
XX	KW	ds.	
XX	OS	Arabidopsis sp.	
XX	PN	WO200179517-A2.	
XX	PD	25-OCT-2001.	
XX	PF	13-APR-2001; 2001WO-US11967.	
XX	PR	13-APR-2000; 2000US-0548971.	
XX	PA	(REGC) UNIV CALIFORNIA.	
XX	PI	Liljegren S, Yanofsky MF;	
XX	PI	WPI; 2002-034365/04.	
XX	DR	Isolated nucleic acids for modulating fruit dehiscence in plants,	
XX	PT	comprises an indehiscent 1 (IND1) polynucleotide sequence -	
XX	PS	Disclosure; Page 50-54; 58pp; English.	
XX	CC	The sequence represents the Arabidopsis dehiscence zone-selective SHP1	
XX	CC	regulatory element. The invention relates to a novel isolated nucleic	
XX	CC	acid encoding an IND1 polypeptide. The polynucleotides of the invention	
XX	CC	provide a means of modulating fruit dehiscence which is useful for	
XX	CC	increased production of crops such as oil seed rape. The IND1 sequences	
XX	CC	can be used to prepare expression cassettes useful in a number of	
XX	CC	techniques, including inhibiting or suppressing expression.	
XX	XX	Sequence 5622 BP; 1853 A; 928 C; 907 G; 1927 T; 7 other;	
XX	XX	Query Match 37.5%; Score 335.8; DB 24; Length 5622;	
XX	XX	Best Local Similarity 99.4%; Pred. No. 2.8e-92;	
XX	XX	Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	558	AAAGATAGCCGAGCGCCAGATTGAATCCGACAGGAGTCCAGTGTGATACAGG	617
Db	5025	ATAGATAGCCGAGCGCCAGATTGAATCCGACAGGAGTCCAGTGTGATACAGG	5084
QY	618	GACGACGTTTACGAATCCGGTGTATCTTCTCATGACGAGTCGAGCATTAATCGGAA	677
Db	5085	GACGACGTTTACGAATCCGGTGTATCTTCTCATGACGAGTCGAGCATTAATCGGAA	5144
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XX	AC	AAT34428;	
XX	DT	01-OCT-1996 (first entry)	
XX	DE	Eucalyptus AGE1 cDNA.	
XX	KW	Eucalyptus; reproductive gene; AGE1; Arabidopsis; agamous gene;	
XX	KW	Antirrhinum; plena gene; sterility; fertility; forest tree;	
XX	KW	transgenic plant; flower development; antisense; ribozyme; ss.	
XX	OS	Eucalyptus globulus.	
XX	FH	Key Location/Qualifiers	
XX	FT	CDS 154..909	
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XX	PN	AU9539013-A.	
XX	PD	30-MAY-1996.	
XX	PF	22-NOV-1995; 95AU-0039013.	
XX	PR	22-NOV-1994; 94AU-0009589.	
XX	PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
XX	PI	Dennis ES, Harcourt RL, Kyoizuka J, Llewellyn D;	
XX	PI	Peacock WJ, Southerton S;	
XX	XX	WPI; 1996-278411/29.	
XX	XX	P-PSDB; AAR99633.	
XX	XX	Eucalyptus reproductive genes - useful for prodn. of sterile	
XX	XX	Eucalyptus trees useful for establishing wood lot plantations or in	
XX	XX	re-forestation projects	
XX	PS	Claim 8; Page 29-30; 60pp; English.	
XX	XX	A cDNA clone (AAT34428), designated AGE1, is analogous to the	
XX	XX	Arabidopsis agamous (AG) and Antirrhinum plena (PLE) flower	
XX	XX	development genes. It was obt'd. by PCR amplification of E.	
XX	XX	globulus cDNA using primers based on homologous regions of the	
XX	XX	Arabidopsis and Antirrhinum genes, followed by a screening of a E.	
XX	XX	globulus library. It codes for a protein, AGE-1 (AAR99633), that	
XX	XX	shows homology to the AG and PLE proteins. AGE1 is very	
XX	XX	highly expressed in mature flower buds. Another cDNA clone,	
XX	XX	AGE2 (AAT34432), was also identified. Antisense or ribozyme	
XX	XX	constructs of AGE, or of PLE2 and SGE genes (see also AAT34426 and	
XX	XX	AAT34429-31), can be used to produce sterile transgenic Eucalyptus	
XX	XX	trees by minimising inflorescence.	

OS	Arabidopsis thaliana.	
PN		
XX	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-0301439.	
XX		
PR	25-FEB-1999;	99US-0121825.
PR	05-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123548.
PR	23-MAR-1999;	99US-0125788.
PR	29-MAR-1999;	99US-0126264.
PR	28-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130891.
PR	28-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132048.
PR	04-MAY-1999;	99US-0132407.
PR	04-MAY-1999;	99US-0132484.
PR	05-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132863.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	18-JUN-1999;	99US-0139457.
PR	17-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
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PR	18-JUN-1999;	99US-0139460.
PR	21-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139819.
PR	23-JUN-1999;	99US-0140353.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	24-JUN-1999;	99US-0140823.
PR	28-JUN-1999;	99US-0140991.
PR	29-JUN-1999;	99US-0140991.

PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144866.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
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PR	20-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
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PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146388.
PR	02-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147935.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
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PR	25-AUG-1999;	99US-0150566.
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PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
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PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
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PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
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PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
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PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.
Query Match 35.9%; Score 322; DB 21; Length 511;		
Best Local Similarity 87.6%; Pred. No. 1.5e-88;		
Matches 352; Conservative 0; Mismatches 50; Indels 0; Gaps 0;		
QY	6	AATGGAGGAAGTGGGAGTAGTCACGAGCGCAGAGTAGTACGAAGAACTAGGAGAGGGAA 65
Db	110	AATGGAGGGTGGTCCGAGTAATGAAGTAGCAGAGCAGCAGAGAGATAGGAGAGGGAA 169
QY	66	AATAGAGATAAGAGAGGATAGAGAACACAAATCGTCAAGTTACTTTCTGCAACGAGC 125
Db	170	GATAGAGATAAGAGAGGATAGAGAACACTACGAATCGTCAAGTCACTTTCTGCAACGAGC 229
QY	126	CAATGGCTTCTCAAGAAAGCTTATGAACCTCTGCTCTGTGTGATCGGAAGTTGCCCT 185
Db	230	CAATGGTTTACTCAAGAAAGCTTATGAGCTCTGCTGCTGTGTGAGCTGAGTTGCTCT 289
QY	186	CGTCATCTTCTCCACTCGTGGCCGTCTATGAGTACGCCAACACACAGTGTGAGGGGTAC 245
Db	290	TGTCATCTTCTCCACTCGAGGCCGTCTACGAGTACGCCAACACACAGTGTGAGAGAAC 349
QY	246	AATTGAAGAGGTACAGAAAGCTTGTTCGATGCCCTCAACCTCTTCCGTCAACGAGC 305
Db	350	AATAGAAAGGTACAAGAAAGCTTGTCTCGAGCCGCTTAACCTCCGACTATCACCGAAGC 409
QY	306	TAATACACAGTACTATCAGCAAGAGCCTTAAGCTTCGGAGGCAGATTCGAGATATCA 365
Db	410	TAATACTCAGTACTATCAGCAAGAGCGCTCTAACTCCGAGACACAGATTCGGACATTCA 469
QY	366	GAATTCAATAGGCATATTGTTGGGAATCACTTGTTTCCTT 407

PS Claim 1; Page 74-75; 92pp; English.

166 TGTGATGCCGAAGTTGCCCTCGTCATCTTCTCCACTCGTGGCCGTCTCTATGAGTACGCC 225

166 TGT

CC The present sequence is that of cDNA encoding *Populus balsamifera*
CC subsp. *trichocarpa* PTAG-2 protein (see AY58657). The PTAG-2 gene (see
CC AAZ57948) is 1 of 4 newly identified floral homeotic genes from this
CC poplar species. PTAG-2 is a homologue of AGAMOUS and is expressed
CC in floral tissue. The invention provides nucleic acid sequences of
CC these 4 *Populus* genes, the corresponding cDNA sequences (see
CC AAZ57942-49) and deduced amino acid sequences (see AY58454-57). It also
CC provides methods of using the genes and cDNA to produce genetically
CC engineered *Populus* species and other trees having modified fertility
CC characteristics, including sterility. Genetic constructs useful in
CC producing these genetically engineered trees include antisense
CC versions of PTAG-2, dominant negative mutants, and constructs useful
CC for sense suppression. Promoter sequences may be used to obtain
CC floral specific expression of genes such as cytotoxins that may be
CC used in genetic ablation strategies to produce trees having modified
CC fertility characteristics, including sterility. Sterile trees
CC allow increased wood yield and a reduction in the production of
CC allergens such as pollen.

XX
SQ Sequence 1115 BP; 342 A; 240 C; 234 G; 299 T; 0 other;
Query Match 34.9%; Score 312.6; DB 21; Length 1115;
Best Local Similarity 73.0%; Pred. No. 1.7e-85;
Matches 402; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 46 AAGAACTAGGAGGAGGAAATAGAGATAAGAGGATAGAGAACACACACAATCGTCAA 105
Db 138 AGGAAGCTGGGGAGGGAAAGGTGGAGATCAAGAGGATCGAGAACACCACCAATCGCCAA 197

Qy 106 GTTACTTTCTCAACAGCAGCAATGGTCTCTCAAGAAAGCTTATGAATCTCTGTCTTG 165
Db 198 GTCACTTTCTCAAAAGCGGAATGGTTGCTCAAGAAAGCCTATGAATATCTGTCTT 257

Qy 166 TGTGATGCCGAAGTTGCCCTCGTCATCTTCTCCACTCTGTGGCCGCTCTATGAGTACGCC 225
Db 258 TGCATGCTGAGGTGTCACATCGTCTTCTCCAGCCGTGGACGCTTTATGAGTACTCT 317

Qy 226 AACACAGCTGTGAGGGTACAAATTCGAAAGGTACAAAGAGCTTGTCCGATGCCGTCAAC 285
Db 318 AACAAATAGTCAATCTACAAATTCGAAAGGTACAAAGGCAATGTCAGATTTCTTCCAAAC 377

Qy 286 CCTCTTCCGTCACGAAGCTAATCTCAGTACTATCAGCAAGAAGCCCTCTAAGCTTCGG 345
Db 378 AACGGTCAAGTTCTTGAAGCCAAATCCTCAGTTCTATCAGCAAGAAGCTGCCAAGCTGCGC 437

Qy 346 AGGCAGATTCGAGATATTCAGAAATTCAGAAATAGGCATATGTTGGGAATCACTTGTCTC 405
Db 438 TCGCAATTTGTAATTTGCAGAAATTCAGAAATAGGCATATGCTGGTGAATCACTTAGTGCA 497

Qy 406 TTGAATTCAGGAATCTCAAAACCTAGAGGACGCTTTGAAAAAGGAATCAGCCGTGTC 465
Db 498 TTGATGTGAAGGAATCTTAAGAGCTTGGAGATTAACCTTGAGAAAGGAATTTGTAGAAT 557

Qy 466 CGCTCCAAAAGAATGAGCTGTAGTGGCAGAGATAGATATATGAGAGAGGGAATG 525
Db 558 CGTTCCAAAAGAATGAGCTGTAGTGGTGTGTTGCTGAATAGTATATGATGAGAGAGGAGAT 617

Qy 526 GAGTTGCAACAAATACATGTACCTGCGAGCAAGATAGCCGAGGCGCAGATTGAAT 585
Db 618 GACTTGCACAAATACCAAGCTTCTCCGAGCAAGATTTGCAGAGAAATGAAAGAACGGA 677

Qy 586 CCGGACCAACA 596
Db 678 CAGCACATGAA 688

RESULT 11
AAF85401
ID AAF85401 standard; cDNA; 1159 BP.
XX
AC AAF85401;
XX
DT 23-JUL-2001 (first entry)

XX Nucleotide sequence of the floral homeotic protein PTAG-2.
DE
XX
XX Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;
KW LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
KW fertility; sterility; ss.
XX
OS *Populus balsamifera*.
XX
FH Key Location/Qualifiers
FT CDS 99..815
FT /tag= a
FT /product= "PTAG-2"
XX
XX CA2319853-Al.
XX
PD 01-APR-2001.
XX
PF 02-OCT-2000; 2000CA-2319853.
XX
PR 01-OCT-1999; 99US-0410464.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
XX
XX WPI: 2001-336098/36.
DR P-PSDB; AAB68438.
XX
PT Novel isolated polynucleotide derived from *Populus* species, useful for
PT producing transgenic plants having modified fertility characteristic,
PT particularly sterility -
XX
XX Claim 25; Page 60-61; 69pp; English.
XX
XX The present sequence encodes a floral homeotic protein, designated
CC PTAG-2, which is derived from *Populus balsamifera* subsp. *trichocarpa*.
CC The specification also describes PTD, PTLF, and PTAG-1 proteins. The
CC floral homeotic proteins are expressed in floral tissues. PTLF is a
CC homologue of LFY and FLORICAULA (FLO), and is expressed in
CC immature inflorescences on which floral primordia are developing. PTD
CC is a homologue of DEFICIENS (DEF), and is strongly expressed in stamen
CC primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
CC homologues of AGAMOUS (AG). The floral homeotic proteins and
CC polynucleotides are useful for producing transgenic plants having
CC modified fertility characteristics, particularly sterility.
XX
SQ Sequence 1159 BP; 386 A; 240 C; 234 G; 299 T; 0 other;
Query Match 34.9%; Score 312.6; DB 22; Length 1159;
Best Local Similarity 73.0%; Pred. No. 1.7e-85;
Matches 402; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 46 AAGAACTAGGAGGAGGAAATAGAGATAAGAGGATAGAGAACACACAATCGTCAA 105
Db 138 AGGAAGCTGGGGAGGGAAAGGTGAGATCAAGCGATCGAGAACACCACCAATCGCCAA 197

Qy 106 GTTACTTTCTGCAACAGCAGCAATGGTCTTCTCAAGAAAGCTTATGAATCTCTGTCTTG 165
Db 198 GTCACTTTCTCAAAAGGCGGAATGGTTGCTCAAGAAAGCCTATGAATATCTGTCTT 257

Qy 166 TGTGATGCCGAAGTTGCCCTCGTCATCTTCTCCACTCTGTGGCCGCTCTATGAGTACGCC 225
Db 258 TGCATGCTGAGGTGTCACATCGTCTTCTCCAGCCGTGGACGCTTTATGAGTACTCT 317

Qy 226 AACACAGTGTGAGGGTACAAATTCGAAAGGTACAAAGAGCTTGTCCGATGCCGTCAAC 285
Db 318 AACAAATAGTCAATCTACAAATTCGAAAGGTACAAAGGCAATGTCAGATTTCTTCCAAAC 377

Qy 286 CCTCTTCCGTCACGAAGCTAATCTCAGTACTATCAGCAAGAAGCCCTCTAAGCTTCGG 345
Db 378 AACGGTCAAGTTCTTGAAGCCAAATCCTCAGTTCTATCAGCAAGAAGCTGCCAAGCTGCGC 437

QY	346	AGGCAGATTCGAGATATTCAAAATCAGAATTAAGCATATTTGGGGGAATCACTTGGTGCC	408
Db	438	TCCGAAAATTCGTAAATTTGCCAGAAATTCAAACAGGAATATGCTGGGTGAATCACTTAGTGCA	497
QY	406	TTGAACATTCGAAGGAACTCAAAAACCTAGAAGGACGCTTTGAAAAAGGAATCAGCGGTGC	465
Db	498	TTGAGTCTGAAGGACTTAAAGACTTTGGAGATNAAAATTGAGNAAGGAATTCGTAGAATT	557
QY	466	CGCTCCAAAAAGAAATGAGCTGTTTAGTGGCAGAGATAGAGTATATGCAGAAGAGGAAAATG	525
Db	558	C GTTCGAAAAAGAAATGAGCTGTTGTTGCTGAAATTCAGTATATGCAGAAGAGGAGATT	617
QY	526	GAGTTCGAACAACATAACATGTACCTCCGAGCAAAAGATACCCCAAGGCCGCCAGATTGAT	585
Db	618	GACTTGCACACCAATACCAGCTTC CGAGCAAAAGATTGCAGAGAAATGAAAGAACGCA	677
QY	586	CCGACCAACGCA	596
Db	678	CAGCACATGAA	688
 RESULT 12 ABK88491			
ID	ABK88491	standard; cDNA; 1159 BP.	
XX	AC	ABK88491;	
XX	DT	07-OCT-2002 (first entry)	
XX	DE	Poplar floral homeotic protein, PTAG-2, cDNA.	
XX	KW	Poplar; ss; gene; plant; DEFICIENS; transgenic; promoter;	
KW	KW	protein transduction domain; floral homeotic gene;	
KW	KW	floral-specific expression; cytotoxin; fertility; sterility;	
KW	KW	PtLF; PTAG-1; PTAG-2.	
XX	OS	Populus balsamifera subsp. trichocarpa.	
XX	FH	Key Location/Qualifiers	
FT	FT	CD5 99..815	
FT	FT	/tag= a	
FT	FT	/product= "PTAG-2"	
XX	PN	US6395892-B1.	
XX	PD	28-MAY-2002.	
XX	PF	01-OCT-1999; 99US-0410464.	
XX	PR	06-APR-1998; 98US-080851P.	
XX	PR	06-APR-1999; 99US-0287700.	
XX	PA	(UYOR-) UNIV OREGON HEALTH SCI.	
XX	PI	Strauss SH, Rottmann W, Brunner A, Sheppard L;	
XX	DR	WPL; 2002-572853/61.	
XX	DR	P-PSDB; ABG30868.	
XX	PT	New protein transduction domain promoter nucleic acid molecule useful	
PT	PT	for producing transgenic plants having modified fertility	
PT	PT	characteristics, particularly sterility -	
XX	PS	Disclosure; Column 77-80; 46pp; English.	
XX	CC	The invention relates to an isolated nucleic acid molecule especially	
CC	CC	protein transduction domain (PTD) promoter: (i) that hybridises under	
CC	CC	wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 %SDS (sodium	
CC	CC	dodecyl sulphate) at 65 plusOC to nucleotides or (ii) comprising 35	
CC	CC	consecutive nucleotides of the PTD gene. PTD is a floral homeotic	
CC	CC	gene and is the homologue of DEFICIENS. Also includes are a recombinant	
CC	CC	nucleic acid comprising the PTD promoter, a cell transformed with	
CC	CC	the recombinant nucleic acid and a transgenic plant comprising the	

CC	transformed cell. The PTD promoter is useful to obtain floral-specific expression of genes such as cytochromes, that are employed in genetic ablation strategies to produce trees having modified fertility characteristics, including sterility. Genetic constructs comprising antisense versions or dominant negative mutants of PTD are useful in producing genetically engineered Poplars and other trees, and for sense CC suppression. Also disclosed are 3 other homeotic genes PTLF, PTAG-1 CC and PTAG-2 (none are defined). The present sequence is the PTAG-2 cDNA.
XX	
SQ	Sequence 1159 BP; 386 A; 240 C; 234 G; 299 T; 0 other;
	Query Match 34.9% Score 312.6; DB 24; Length 1159; Best Local Similarity 73.0%; Pred. No. 1.7e-85; Matches 402; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
QY	46 AAGAAACTAGGAGAGGGAAAATAGAGATAAAGAGGATAGAGAACAACAAATCGTCAA 105
DB	138 AGGAAGCTGGGGAGGGAAAGGTGGAGATCAAGCGGATCGAGAACACCACCAATCGCCAA 197
QY	106 GTTACTTTCTGCANACGACGAANTGGTCTCTCAAGAAAGCTTATGACTCTCTCTCTTG 165
DB	198 GTCACTTTCTGCANAGGGGGAATGGTTGCTCAAGAAAGCCTATGAATTATCTTGTTCTT 257
QY	166 TGTGATGCCGAAGTTGCCCTCGTCACTCTTCACACTCGTGGCCGCTCTATGAGTAGGCC 225
DB	258 TGCGATGCTGAGGTTGCACATCATCGTCTCTCCAGCGGTGGACGCCCTTATGAGTACTCT 317
QY	226 AACACAGCTGTGAGGGGTACAATTTGAAGGTACAAGAAAGCTTGTTCGGATGCCGTCAAC 285
DB	318 AACAAATGTTGTCAAATCTTACAATTTGAAGGTACAAAAGGCATGTGCAGATTCTTCCAAC 377
QY	286 CTCTCTCCGTCACCGAAGCTTAATACTCAGTACTATCAGCAAGAAGCCTCTFAAGCTTCGG 345
DB	378 AACGGGTCAGTTTCTGAAGCCATGCTCAGTCTTATCAGCAAGAAGCTGCCAAGCTGGCC 437
QY	346 AGGCAGATTGAGATATTCAGAAATCAAAATAGGCATATGTGTGGGAATCACTTGGTTCC 405
DB	438 TCGCAAAATGGTAAATTTTCAGAAATTCAAACAGGAATATGCTGGGTGAATCACTTAGTGCA 497
QY	406 TTGAAGTTCAGGAAGCTCAAAAACCTAGAAGAGCTCTTGA AAAAGGAATCAGCCGTGTC 465
DB	498 TTGAGTTGAAGGAACCTTAAGAGCTTGGAGATAAACTTGAAGAAGNATTTGTTAGAAATT 557
QY	466 CGCTCCAAAAAGATGAGCTGTTAGTGGCAGAGATAGATATATCGAAGAGGGAATG 525
DB	558 CGTTCGAAAAAGATGAGCTGTTGTTGCTGAAATTTGAGTATATCGAAGAGGGAGATT 617
QY	526 GAGTTGCACACATACATGCTAGCTCGGACCAAGATAGCCGAGGCCCGACGATTGAAT 585
DB	618 GACTTGCACACAAATACCAAGCTTCCGAGCAAGATTTCGAGAGATGAAGAAGGCGA 677
QY	586 CCGGACCCAGCA 596
DB	678 CAGCACATGAA 688
	RESULT 13 AAC45357 ID AAC45357 standard; DNA; 511 BP. XC AAC45357; AC AAC45357; XX DT 18-OCT-2000 (first entry) XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46222. XX KW Hybridisation assay; genetic mapping; gene expression control; KW protein identification; signal transduction pathway; KW metabolic pathway; promoter; termination sequence; ss. XX OS Arabidopsis thaliana. XX PN EP1033405-A2.

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XX	PR	02-JUL-1999;	99US-0142055.
PD	PR	06-JUL-1999;	99US-0142390.
XX	PR	08-JUL-1999;	99US-0142803.
PF	PR	09-JUL-1999;	99US-0142920.
XX	PR	12-JUL-1999;	99US-0142977.
PR	PR	13-JUL-1999;	99US-0143542.
PR	PR	14-JUL-1999;	99US-0143624.
PR	PR	15-JUL-1999;	99US-0144005.
PR	PR	16-JUL-1999;	99US-0144085.
PR	PR	16-JUL-1999;	99US-0144086.
PR	PR	19-JUL-1999;	99US-0144325.
PR	PR	19-JUL-1999;	99US-0144331.
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PR	PR	19-JUL-1999;	99US-0144333.
PR	PR	19-JUL-1999;	99US-0144334.
PR	PR	19-JUL-1999;	99US-0144335.
PR	PR	20-JUL-1999;	99US-0144352.
PR	PR	20-JUL-1999;	99US-0144632.
PR	PR	20-JUL-1999;	99US-0144632.
PR	PR	21-JUL-1999;	99US-0144884.
PR	PR	21-JUL-1999;	99US-0144814.
PR	PR	21-JUL-1999;	99US-0145086.
PR	PR	21-JUL-1999;	99US-0145088.
PR	PR	22-JUL-1999;	99US-0145085.
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PR	PR	22-JUL-1999;	99US-0145192.
PR	PR	23-JUL-1999;	99US-0145145.
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PR	PR	23-JUL-1999;	99US-0145224.
PR	PR	26-JUL-1999;	99US-0145276.
PR	PR	27-JUL-1999;	99US-0145913.
PR	PR	27-JUL-1999;	99US-0145918.
PR	PR	27-JUL-1999;	99US-0145919.
PR	PR	28-JUL-1999;	99US-0145951.
PR	PR	02-AUG-1999;	99US-0146386.
PR	PR	02-AUG-1999;	99US-0146388.
PR	PR	02-AUG-1999;	99US-0146389.
PR	PR	03-AUG-1999;	99US-0147038.
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PR	PR	06-AUG-1999;	99US-0147416.
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PR	PR	09-AUG-1999;	99US-0147935.
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PR	PR	16-AUG-1999;	99US-0149368.
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PR	PR	20-AUG-1999;	99US-0149722.
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PR	PR	25-AUG-1999;	99US-0150566.
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PR	PR	01-SEP-1999;	99US-0151930.
PR	PR	07-SEP-1999;	99US-0152363.
PR	PR	10-SEP-1999;	99US-0153070.
PR	PR	13-SEP-1999;	99US-0153758.
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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
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PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
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Query Match 34.8%; Score 311.6; DB 21; Length 511;
Best Local Similarity 87.4%; Pred. No. 2.3e-85;
Matches 353; Conservative 0; Mismatches 49; Indels 2; Gaps 1;

QY 6 AATGGAGGAGTGGGAGTAGTCACGACGAGAGTAGCAAGAACTAGGAGAGGGAA 65
DB 108 AATGAGGGTGGTGGCAGTAATGAGTAGCAGAGCAGCAGAGATAGGAGAGGAA 167
QY 66 AATAGAGATAAGAGATAGAGAACACACAAATCGTCAAGTTACTTTCTGCAACGACG 125
DB 168 GATAGAGATAAGAGATAGAGAACACTAGCAATCGTCAAGTCACTTTCTGCAACGACG 227
QY 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTCTGTGTGATCCGGAAGTTGCCCT 185
DB 228 CAATGGTTTACTCAAGAAAGCTTATGAACCTCTCTGTCTGTGTGATCCGGAAGTTGCCCT 287
QY 186 CQTGATCTTCTCCACTCGTGGCGCTCTCTATGATAGCGCAACAACTAGTGTGAGGGGTAC 245
DB 288 TGCTCATCTTCTCCACTCGAGGCGCTCTCTACGAGTAGCGCAACAACTAGTGTGAGAGGAAC 347
QY 246 AATTGAAAGGTACAAAGAGCTTGTTCGGATGCGGTCAACCCCTCTCCGTCACCGAAGC 305
DB 348 AATGAAAGGTACAAAGAGCTTGTTCGGATGCGGTCAACCCCTCTCCGTCACCGAAGC 407
QY 306 TAATACTC--AGTACTATCAGCAAGAGCCTCTAAGCTTCGGAGGCGAGATTCGAGATATT 363
DB 408 TAATACTCAGACTACTATCAGCAAGAGGCGTCTAAACTCCGGAGACAGATTCGGACATT 467
QY 364 CAGAAATCAAAATAGGCATATTGTTGGGGGAATCACTTGGTTCCTT 407
DB 468 CAGAAATTTGAACAGACACATCTTGTGGTGAATCTCTTGGTTCCTT 511

RESULT 14
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ID AAF85399 standard; cDNA; 723 BP.
XX
AC AAF85399;
XX
DT 23-JUL-2001 (first entry)
XX
Nucleotide sequence of the floral homeotic protein PTAG-1.
XX
Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;
KW LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
KW fertility; sterility; ss.
XX
OS Populus balsamifera.
XX
FH Key Location/Qualifiers
CDS 1..723
FT /*tag= a
FT /product= *PTAG-1*
XX
CA2319853-A1.
XX
PD 01-APR-2001.
XX
PF 02-OCT-2000; 2000CA-2319853.
XX
PR 01-OCT-1999; 99US-0410464.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
XX
DR WPI; 2001-336098/36.
XX
DR P-ESDB; AAB68437.
XX
Novel isolated polynucleotide derived from Populus species, useful for
producing transgenic plants having modified fertility characteristic,
particularly sterility -
XX
Claim 25; Page 55-56; 69pp; English.
XX
The present sequence encodes a floral homeotic protein, designated
PTAG-1, which is derived from Populus balsamifera subsp. trichocarpa.
The specification also describes PTD, PTLF, and PTAG-2 proteins. The
floral homeotic proteins are expressed in floral tissues. PTLF is a
homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in
immature inflorescences on which floral primordia are developing. PTD
is a homologue of DEFICIENS (DEF), and is strongly expressed in stamen
primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
homologues of AGAMOUS (AG). The floral homeotic proteins and
polynucleotides are useful for producing transgenic plants having
CC modified fertility characteristics, particularly sterility.
XX
Sequence 723 BP; 226 A; 147 C; 175 G; 175 T; 0 other;

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DB 40 AGGAAGCTGGGAAGGGGAAGGTGGAGATCAAGCGGATCGAGAACACCAATCGGCAA 99
QY 106 GTTACTTTCTGCAACGACGCAATGCTTCTCTCAAGAAAGCTTATGAACCTCTGTCTTG 165
DB 100 GTCACCTTCTGCAAGAGCGCAGTGTGTTGCTCAAGAAAGCTTATGATTTCTT 159
QY 166 TGTGATGCCGAAGTTCCTTCGTCATCTTCTCCACTCGTGGCGCTCTCTATGATAGTACC 225
DB 160 TGGCATGCTGAGGTTCGACTCATCTTCTCTAGCGCGGTGCGCTTATGATAGTACTCT 219
QY 226 AACAACTAGTGTGAGGGGTACAAATTGAAAGGTACAAAGAAAGCTTGTTCGATCGGTCAAC 285
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220 AACGATAGTGTCAAAATCAAAATGAGAGGTACAAAAGGCATCTGCAGATCTTCAAAAC 279
 286 CPTCCCTCCGTCACCGAAGCTAATACTACTAGTATATCAGCAAGAGCTCTTAAGCTTCGG 345
 280 ACNCGGTCTGTTCTGAGGCAATGCTCAGTACTACCAAGCAAGAGCTGCCAAGCTGGT 339
 346 AGCAGATTCGAGATATTCAGAAATTCAGAAATAGGCAATTTGTTGGGGAATCACTTGGTTCC 405
 340 TCCCAAAATTTGTAATTTGCAGAAATTCAGCAAGGCATATGCTGGGTGAAGCGCTTAGTTCA 399
 406 TTGAACCTTCAAGCACTCAAAACCTAGAGAGGCTCTTGAAAAAGGAATCAGCGCTGTC 465
 400 TTGAGTGTGAAGGAATTAAGAGTTTGGAAATACGACTTTGAGAAGGAATAGCAGAAAT 459
 466 CGCTCCAAAAGAAATGAGCTGTAGTGGCAGAGATAGAGTATATGCAGAGAGGGAATG 525
 460 CGTTCCAAAAAGAAATGAGCTGTTGTTGCAAGAAATCGAGTATATGCAGAGAGGAGGT 519
 526 GAGTTGCACACAAATACATGTACCTCGGAGCAAGATAGCCGAAGGCGCCAGA 579
 520 GACTTGCAACAATAACCAAGCTTCTCCGAGCAAAAGATTTTCAGAGAAATGAAAGA 573

RESULT 15
 AA257947
 ID AA257947 standard; cDNA; 1201 BP.
 XX AC AA257947;
 XX 11-APR-2000 (first entry)
 DE Poplar floral homeotic gene PTAG-1 cDNA.
 XX KW Poplar; PTAG-1; floral homeotic gene; transgenic plant; sterility;
 XX KW fertility; ss.
 XX OS Populus balsamifera subsp. trichocarpa.
 XX FH Key Location/Qualifiers
 XX CDS 196..921
 FT FT /*tag= a
 FT FT /note= "the coding region is also specifically
 XX claimed in Claim 1"
 XX CA2227940-A1.
 XX 06-OCT-1999.
 XX 07-APR-1998; 98CA-2227940.
 XX 06-APR-1998; 98US-0080851.
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 XX Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;
 XX WPI; 2000-106662/10.
 XX P-PSDB; AAY58656.
 XX Nucleic acid from Populus trichocarpa genes, useful for producing
 XX transgenic plants, particularly trees, with modified fertility
 XX characteristics such as sterility -
 XX Claim 1; Page 64-66; 92pp; English.
 XX The present sequence is that of cDNA encoding Populus balsamifera
 XX subsp. trichocarpa PTAG-1 protein (see AAY58656). The PTAG-1 gene (see
 XX AA257946) is 1 of 4 newly identified floral homeotic genes from this
 XX poplar species. PTAG-1 is a homologue of AGAMOUS and is expressed
 XX in floral tissue. The invention provides nucleic acid sequences of
 XX these 4 Populus genes, the corresponding cDNA sequences (see
 XX AA257942-49) and deduced amino acid sequences (see AAY58454-57). It also

CC provides methods of using the genes and cDNA to produce genetically
 CC engineered Populus species and other trees having modified fertility
 CC characteristics, including sterility. Genetic constructs useful in
 CC producing these genetically engineered trees include antisense
 CC versions of PTAG-1, dominant negative mutants, and constructs useful
 CC for sense suppression. Promoter sequences may be used to obtain
 CC floral specific expression of genes such as cytotoxins that may be
 CC used in genetic ablation strategies to produce trees having modified
 CC fertility characteristics, including sterility. Sterile trees
 CC allow increased wood yield and a reduction in the production of
 CC allergens such as pollen.
 XX SQ Sequence 1201 BP; 354 A; 251 C; 257 G; 339 T; 0 other;
 Query Match 34.1%; Score 305.2; DB 21; Length 1201;
 Best Local Similarity 73.2%; Pred. No. 3.3e-83;
 Matches 391; Conservative 0; Mismatches 143; Indels 0; Gaps 0;
 QY 46 AAGAACTAGGGAGAGGAAATAGAGATAAGAGGATAGAGAACACACAAATTCGTCAA 105
 DB 235 AGGAAGCTGGGAAGGGAAGGTGGAGATCAAGCGGATCGAAGAACACCAATTCGCCAA 294
 QY 106 GTTACTTTCTGCAACGACGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTTG 165
 DB 295 GTCACTTTCTGCAAAAGGCGCAGTGGTCTGCTCAAGAAAGCTTACGAATTATCTGTTCT 354
 QY 166 TGTGATGCCGAAGTTGCCCTCGTCATCTTCTCCACCTCGTGGCGGTCTCTATGATAGCC 225
 DB 355 TGGATGCTGAGGTTCGACTCATCTCTCTAGCGCGGTGCGCTTATGACTACTCT 414
 QY 226 AACACAGTGTGAGGGGTACAAATTGAAAGGTACAAAGAAAGCTTGTCCGATGCCGTCAAC 285
 DB 415 AAGGATAGTGTCAATCAACAATTGAGAGGTACAAAAGGCATCTGCAGATTTCTTCAAC 474
 QY 286 CCTCCTTCGTCACCGAAGCTAATCTACTACTATCAGCAAGAGCTCTTAAGCTTCGG 345
 DB 475 ACTGGGTCTGTTTCTGAAGCCAATGCTCAGTACTACCGCAAGAGCTGCCAAGCTGGT 534
 QY 346 AGGCATTCGAGATATTCAGAAATTCAGAAATAGGCATATTTGGGGAATCACTTGGTTCC 405
 DB 535 TCCCAAAATTTGTAATTTGCAGAAATTCAGAGGCATATGCTGGTGAAGCGCTTAGTTCA 594
 QY 406 TTGAACCTTCAAGCACTCAAAAACCTAGAGGAGCTTTGAAAAAGGAATCAGCGCTGTC 465
 DB 595 TTGAGTGTGAAGGAAGCTTAAGAGTTTGGAAATACGACTTGAGAAAGGAATTAAGCAGAA 654
 QY 466 CGCTCCAAAAGAAATGAGCTGTTAGTGGCAGAGATAGATATATGCAGAGAGGGAATG 525
 DB 655 CGTTCCAAAAGAAATGAGCTGTTGTTGCAAGAAATCGATATATGCAGAGAGGAGGT 714
 QY 526 GAGTTGCACACAAATACATGTACCTCGGAGCAAGATAGCCGAAGGCGCCAGA 579
 DB 715 GACTTGCAACAATAACCAAGCTTCTCCGAGCAAAAGATTTTCAGAGAAATGAAAGA 768

Search completed: February 2, 2003, 08:18:57
 Job time : 243.706 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 08:19:29 ; Search time 2453.74 Seconds
(without alignments)
10627.107 Million cell updates/sec

Title: US-09-978-382A-3

Perfect score: 896

Sequence: 1 ggatcaatggaggaggtgg.....actgtgtttttttgttcca 896

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_htg:*

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6: gb_pat:*

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11: gb_sts:*

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17: em_hum:*

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20: em_om:*

21: em_or:*

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32: em_htg_other:*

33: em_htg_mus:*

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35: em_htg_rod:*

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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2	895	99.9	895	8	ATHAGL1A	M5550 Arabidopsis
3	887	99.0	1202	8	AY086196	AY086196 Arabidops
4	634.4	70.8	789	8	AY036062	AY036062 Brassica
5	536.8	59.9	959	6	ARI138348	ARI138348 Sequence
6	536.8	59.9	963	8	ATHAGL5A	M5553 Arabidopsis
7	344.8	38.5	1125	6	AR003863	AR003863 Sequence
8	344.8	38.5	1125	8	TOBNAG1A	L23925 Nicotiana t
9	343.2	38.3	1084	8	TOMTAG1A	L26295 Lycopersico
10	335.8	37.5	5622	6	ARI138345	ARI138345 Sequence
11	335.8	37.5	5622	6	AX320929	AX320929 Sequence
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14	325.6	36.3	1214	8	PHPMADS3	X72912 P.hybrida p
15	319.8	35.7	1160	8	AF265562	AF265562 Vitis vin
16	319.2	35.6	1065	8	AB025643	AB025643 Rosa rugo
17	318	35.5	1224	8	PETRHP	L33973 Petunia inf
18	316.4	35.3	956	8	PHFBP6A	X68675 P.hybrida f
19	313.4	35.0	1080	8	PGORFGAG2	Z46612 P.ginseng g
20	305.4	34.1	1073	8	S53900	S53900 ple-plena l
21	297.2	33.2	1197	8	AF103903	AF103903 Liquidamb
22	295.6	33.0	1082	8	AF265554	AF265554 Cucumis s
23	294.8	32.9	1165	8	BPE252071	AJ252071 Betula pe
24	292.8	32.7	1128	8	DCA271150	AJ271150 Daucus ca
25	292.6	32.7	967	8	CSCUS1	X97801 C.sativus C
26	292.4	32.6	1179	8	AF027376	AF027376 Corylus a
27	291	32.5	1000	8	AF022378	AF022378 Cucumis s
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32	289.8	32.3	1142	8	AF022377	AF022377 Cucumis s
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34	284.4	31.7	1097	6	AR003862	AR003862 Sequence
35	284.4	31.7	1098	8	BNABAG1X	M99415 Brassica na
36	284.4	31.7	1345	8	CSA312773	AJ312773 Cucumis s
37	283.8	31.7	763	8	AY083173	AY083173 Gossypium
38	282.4	31.5	905	8	ATU20182	U20182 Arabidopsis
39	282.4	31.5	1057	8	AY087201	AY087201 Arabidops
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43	276.4	30.8	977	8	AF286649	AF286649 Cucumis s
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ALIGNMENTS

RESULT 1
ARI138347
LOCUS
DEFINITION Sequence 5 from patent US 6198024.
ACCESSION ARI138347
VERSION ARI138347.1 GI:14479856
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 896)
AUTHORS Yanofsky,M.F. and Ferrandiz,C.
TITLE Seed plants characterized by delayed seed dispersal
JOURNAL Patent: US 6198024-A 5 06-MAR-2001;
FEATURES Location/Qualifiers

ARI138347
Sequence 5 from patent US 6198024.
ARI138347
GI:14479856
Unknown.
Unclassified.
1 (bases 1 to 896)
Yanofsky,M.F. and Ferrandiz,C.
Seed plants characterized by delayed seed dispersal
Patent: US 6198024-A 5 06-MAR-2001;
Location/Qualifiers

ARI138347
Sequence 5 from patent US 6198024.
ARI138347
GI:14479856
Unknown.
Unclassified.
1 (bases 1 to 896)
Yanofsky,M.F. and Ferrandiz,C.
Seed plants characterized by delayed seed dispersal
Patent: US 6198024-A 5 06-MAR-2001;
Location/Qualifiers

PAT 16-JUN-2001

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LOCUS

QY	121	CGACGCAATGGCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATGCCGAAGTT	180
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QY	241	GSTACAATTGAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCTCTCTCGGTACC	300
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QY	601	TCGAGTGTATACAGGACGACAGTTTACGAATCCGGTGTATCTTCTCATGACCACTCG	660
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ACCESSION	AY086196		
VERSION	AY086196.1	GI:21404906	
KEYWORDS	FLI_CDNA.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.		
REFERENCE	1 (bases 1 to 1202)		
AUTHORS	Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.		
TITLE	Full-length messenger RNA sequences greatly improve genome annotation		
JOURNAL	Genome Biol.		
REFERENCE	2 (bases 1 to 1202)		
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and		

Feldmann,K.			
TITLE	Full-length cDNA from Arabidopsis thaliana		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1202)		
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA		
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.		
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	/product="shatterproof 1 (SHP1)/ agamous-like 1 (AGL1)"		
	/protein_id="AA064275.1"		
	/db_xref="GI:21592324"		
	/translation="MEEGSSHDSESSKLGRIKRIENTTNRVTFCKRRNGLL KAYELSLVCDAEVALVIFSTRGLRYEYANNVPKGIERYKKACDAVNPSPVTEANT QYQQEASKLRQIDIONSNRHIVGESLSLNFKEKLEGRLEKSLRVRKRNEL LVAYEYQKREMELOHNNMYLRKAKLGNLPDQOESSYIQGTTTYESVSSHDQS QYNNRYIPVNLEPNQOFGSDQPPQLV"		
BASE COUNT	397 a 238 c 248 g 319 t		
ORIGIN			
Query Match	99.0%; Score 887; DB 8; Length 1202;		
Best Local Similarity	100.0%; Pred. No. 1.7e-233;		
Matches	887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	316	GGATCAATGGAGGAGGTGGAGTAGTCACGACGACAGAGTAGCAAGAACTAGGGAGA	375
QY	61	GGGAAATAGAGATAAGAGGATAGAGACACAACTCGTCAAGTTACTTTCTGAAA	120
Db	376	GGGAAATAGAGATAAGAGGATAGAGACACAACTCGTCAAGTTACTTTCTGAAA	435
QY	121	CGACCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATGCCGAAGTT	180
Db	436	CGACCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATGCCGAAGTT	495
QY	181	GCCCTCGTCATCTTCTCCACTCGTGGCCGCTCTATGAGTACGCCAACACAGTGTGAGG	240
Db	496	GCCCTCGTCATCTTCTCCACTCGTGGCCGCTCTATGAGTACGCCAACACAGTGTGAGG	555
QY	241	GGTACAATTGAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCTCTCTCGGTACC	300
Db	556	GGTACAATTGAAGGTACAGAAAGCTTGTTCGGATGCCGTCAACCTCTCTCGGTACC	615
QY	301	GAAGCTAATCTACGTACTATCAGCAAGAGCTCTAAGCTTCGGAGCAGATTCGAGAT	360
Db	616	GAAGCTAATCTACGTACTATCAGCAAGAGCTCTAAGCTTCGGAGCAGATTCGAGAT	675
QY	361	ATTCTAGATTCAATAGGCATATTGTTGGGGAATCACTTGGTTCTTGAACCTCAAGGAA	420

Db 676 ATTGAGAAATTCAAATAGGCATATGTTGGGAAATCACTTGGTCTCTTCAACTTCAAGAA 735
QY 421 CTCAAAACCTAGAGGACGCTTCTGAAAAAGGAATCAGCCGTGTCGGCTCCAAAAAGAA 480
Db 736 CTCAAAACCTAGAGGACGCTTCTGAAAAAGGAATCAGCCGTGTCGGCTCCAAAAAGAA 795
QY 481 GAGGTGTTAGTGGCAGAGATAGAGTATATGAGAGAGGGAAATGGAGTTGCAACACAA 540
Db 796 GAGCTGTTAGTGGCAGAGATAGAGTATATGAGAGAGGGAAATGGAGTTGCAACACAA 855
QY 541 AACATGTACCTGCCAGCAAGATAGCCGAGCGCCAGATTGAATCCGAGCAGCAGGAA 600
Db 856 AACATGTACCTGCCAGCAAGATAGCCGAGCGCCAGATTGAATCCGAGCAGCAGGAA 915
QY 601 TCGAGTGTATACAGGAGCAGCAGTGTACGAATCCGGTGTATCTTCTCATGACCACTCG 660
Db 916 TCGAGTGTATACAGGAGCAGCAGTGTACGAATCCGGTGTATCTTCTCATGACCACTCG 975
QY 661 CAGCATTAATCGGAACCTATATCCGGTGAACCTCTTGAACCGAATCAGCAATCTCC 720
Db 976 CAGCATTAATCGGAACCTATATCCGGTGAACCTCTTGAACCGAATCAGCAATCTCC 1035
QY 721 GCCAAGACCAACCTCTCTTCAACTTGTGAACCTCAAAACATGATACTGTTCTTCC 780
Db 1036 GCCAAGACCAACCTCTCTTCAACTTGTGAACCTCAAAACATGATACTGTTCTTCC 1095
QY 781 CCTCATACGATTAAGAGAGAGAGAGAGTTCATTTATATTTATACGCGACTGTGT 840
Db 1096 CCTCATACGATTAAGAGAGAGAGAGAGTTCATTTATATTTATACGCGACTGTGT 1155
QY 841 ATTCATAGTTTGTCTTAATATGATAATACAAACTGTTGTTTC 887
Db 1156 ATTCATAGTTTGTCTTAATATGATAATACAAACTGTTGTTTC 1202

RESULT 4
AY036062 789 bp mRNA linear PLN 01-DEC-2001
LOCUS Brassica napus SHATTERPROOF1 (BnSHP1) mRNA, complete cds.
DEFINITION AY036062
ACCESSION AY036062
VERSION AY036062.1 GI:17223669
KEYWORDS
SOURCE Brassica napus.
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 789)
Pylatuik,J.D., Davis,A.R. and Bonham-Smith,P.C.
Isolation of the coding region of BnSHP by RT-PCR
Unpublished
REFERENCE 2 (bases 1 to 789)
Pylatuik,J.D., Davis,A.R. and Bonham-Smith,P.C.
Direct Submission
TITLE Submitted (17-MAY-2001) Biology, University of Saskatchewan, 112
JOURNAL Science place, Saskatoon, SK S7N 5E2, Canada
LOCATION/Qualifiers
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1. 789
/organism="Brassica napus"
/db_xref="taxon:3708"
1. .789
/gene="BnSHP1"
/note="genomic sequence found in GenBank Accession Number
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1. .39
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40. .789
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/protein_id="AAK62033.1"
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/translation="MDEGGSSHDAESSKKIGRKIEIKRIENTTNRQVTFCKRRNGLL
KKAVLSVLCDAEVALVIFSTRGLLYEASNSVKGTIERVKKKACSDAVNPPTVEANT
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LVAEIEYMKREMLQHVNMYLDRAKIEQARLNPEQHGSGVIGCTAYESGLSSSHDQ
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BASE COUNT 245 a 159 c 193 g 192 t

Query Match 70.8%; Score 634.4; DB 8; Length 789;
Best Local Similarity 90.9%; Pred. No. 7.2e-164;
Matches 687; Conservative 0; Mismatches 66; Indels 3; Gaps 1;
QY 1 GGATCAATGGAGGAAGTGGGAGTAGTCAGCAGCGCAGAGTAGCAAGAACTAGGAGGA 60
Db 34 GAAGCAATGGATGAAGTGGGAGTAGTCAGCAGTAGCAGAGTAGCAAGAACTAGGAGGA 93
QY 61 GGGAAATAGAGATAAAGAGGATAGAGAACACAACTGTCAGTCTTCTGCAAGTTACTTTCTGCAAA 120
Db 94 GGAAGATAGAGATAAAGAGGATAGAGAACACAACTGTCAGTCTTCTGCAAGTTACTTTCTGCAAA 153
QY 121 CGACGCAATGGTCTTCTCAAGAAAGCTTATGAATCTCTCTGTTCTGTCAGTCTGTCGCGAAGTT 180
Db 154 CGACGCAATGGTCTTCTCAAGAAAGCTTATGAGCTCTCTGTTCTGTCAGTCTGTCGCGAAGTT 213
QY 181 GCCTCTGTCATCTTCTCCACTCTGCGCCGTCTCTATGAGTACGCCAACACAGTGTGAGG 240
Db 214 GCCTCTGTTATCTTCTCCACTCTGCGCCGTCTTATGAGTACGCCAACACAGTGTGAGG 273
QY 241 GGTACAATTTGAAGGTACAGAAAGCTTGTTCGATGCCGTCAACCCCTCCCTTCGTCACC 300
Db 274 GGTACAATTTGAAGGTACAGAAAGCTTGTTCGATGCCGTTCGTCGTCGTCGTCGTCGTCGTC 333
QY 301 GAAGCTAATTAATCAGTACTATCAGCAAGAGCCCTCTAAGCTTCGAGGAGCAGATTTCGAGAT 360
Db 334 GAAGCTAATTAATCAGTACTATCAGCAAGAGCCCTCTAAGCTTCGAGGAGCAGATTTCGAGAT 393
QY 361 ATTCAGAAATTCAAATAGGCATATGTTGGGAAATCACTTGGTCTCTTCAACTTCAAGAA 420
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QY 481 GAGCTGTAGTGGCAGAGTAGAGTATATGAGAGAGGGAAATGGAGTTGCAACACAA 540
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QY 541 ACATGTACCTGCCAGCAAGATAGCCGAGCGCCAGATTGAATCCGAGCAGCAGGAA 600
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QY 601 TCGAGTGTATACAGGAGCAGCAGTTCAGAAATCCGGTGT---ATCTTCTCATGACCAAG 657
Db 634 TCCGCTGTATACAGGAGCAGCGGCTTATGAGTCCGGTCTGCTCTTCTCTCATGATCAG 693
QY 658 TCGCAGCATTAATACCGGAATATATTCGCGTGAACCTCTTGAACCGCAATCAGCAATTC 717
Db 694 TCGCAGCATTAATACCGGAATATATTCGCGTGAACCTCTTGAACCGCAATCAGCAATTC 753
QY 718 TCCGCCCAAGACCAACCTCTCTTCAACTTGTGTA 753
Db 754 TCCGGTCAAGACCAACCTCTCTTCAACTTGTGTA 789

RESULT 5
ARI138348 LOCUS 959 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 7 from patent US 6198024.
ACCESSION ARI138348
VERSION ARI138348.1 GI:14479857
KEYWORDS
SOURCE Unknown.

RESULT 6
ATHAGL5A
LOCUS .
DEFINITION
Arabidopsis thaliana transcription factor (AGL5) mRNA, complete
963 bp
linear
PLN 27-APR-1993

Db 531 CGATCCAAAAGAAATGAGCTGTTGTTGCTGAAATGTGAGTATATGCGAAGAGGGAAGCTT 590

QY 526 GAGTTGCAACACATAACATGCTAGCTCGGAGCAAAAGATAGCCGAGGCCGCCAGATTGAAT 585

Db 591 GATTACACAAACAAATCAGTACTCTGAGAGCAAAAGATTGCTGAAACTGAGAGAGCTCAG 650

QY 586 CCGGACAGCAGGAATCGAGTGTGATACAAGGAGCAGCAAGTTTACGAATCCGGTGTATCT 645

Db 651 CATCAGATCATGAGAGATGAATCTTGATGCCAGGGAGTTCATCAAACTATCATGAGCTTGTG 710

QY 646 TCTCATGACCAGTCGCGAGCAATTAATAATCGGAACATATATCCGGTGAACCTTCTTGAACCG 705

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QY 706 ATCAGCAATTTCTCGGCGAAGACCAACCTCTCTTCAACTTGTGTAA 753

Db 768 AACAACTTACCCTAGACAGAACCAACCCCTATTCACTAGTCTAA 815

RESULT 10

ARI138345

LOCUS

DEFINITION Sequence 3 from patent US 6198024.

ACCESSION ARI138345

VERSION ARI138345.1 GI:14479854

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 5622)

Yanofsky,M.F. and Ferrandiz,C.

TITLE Seed plants characterized by delayed seed dispersal

JOURNAL Patent: US 6198024-A 3 06-MAR-2001;

FEATURES

Location/Qualifiers

1. .5622

Source

BASE COUNT 1853 a 928 c 907 g 1927 t 7 others

ORIGIN

Query Match 37.5%; Score 335.8; DB 6; Length 5622;

Best Local Similarity 99.4%; Pred. No. 1.8e-81;

Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 558 AAAGATAGCCGAAGCGCCAGATTGAATCCGGACAGCAGGAATCGAGTGTGATACAAGG 617

Db 5025 ATAGATAGCCGAAGCGCCAGATTGAATCCGGACAGCAGGAATCGAGTGTGATACAAGG 5084

QY 618 GACGACAGTTTACGAATCCGGTGTATCTTCTCATGACGAGTCGCAGCATTAATCGGAA 677

Db 5085 GACGACAGTTTACGAATCCGGTGTATCTTCTCATGACGAGTCGCAGCATTAATCGGAA 5144

QY 678 CTATATTCGGGTGAACCTTCTTGAACCGAATCAGCAATTTCTCGGCCAAGACCAACTCC 737

Db 5145 CTATATTCGGGTGAACCTTCTTGAACCGAATCAGCAATTTCTCGGCCAAGACCAACTCC 5204

QY 738 TCTTCAACTTGTGTAACCTCAAAACATGATAACTTGTTCCTCCCTCATACGATTAGA 797

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QY 858 TAATAATGATAATAACAAAACCTGTGTTTCTTTCCTTCA 896

Db 5325 TAATAATGATAATAACAAAACCTGTGTTTCTTTCCTTAA 5363

RESULT 12

ATT20N10

LOCUS

DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone T20N10.

ACCESSION AL353032

VERSION AL353032.1 GI:7630060

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 90273)

D'Angelo,M., Vezzi,A., Modesto,D., Pigazzi,M., Valle,G., Mewes,H.W., Rudd,S., Lemcke,K., Mayer,K.F.X., Quetier,F. and Salanoubat,M.

Unpublished

2 (bases 1 to 90273)

EU Arabidopsis sequencing, project.

REFERENCE

AUTHORS

JOURNAL

TITLE Direct Submission

AUTHORS Submitted (19-APR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de

JOURNAL Coordinator: Marcel Salanoubat and Francis Quetier, Groupement

AX320929.1 GI:17902476

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1

Liljegren,S. and Yanofsky,M.F.

Control of fruit dehiscence in arabidopsis by indehiscen1 genes

Patent: WO 01/9517-A 5 25-OCT-2001;

The Regents of the University of California (US)

Location/Qualifiers

1. .5622

Source

organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

/note="SHATTERPROOF1 (SHPL) genomic"

BASE COUNT 1853 a 928 c 907 g 1927 t 7 others

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Query Match 37.5%; Score 335.8; DB 6; Length 5622;

Best Local Similarity 99.4%; Pred. No. 1.8e-81;

Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 558 AAAGATAGCCGAAGCGCCAGATTGAATCCGGACAGCAGGAATCGAGTGTGATACAAGG 617

Db 5025 ATAGATAGCCGAAGCGCCAGATTGAATCCGGACAGCAGGAATCGAGTGTGATACAAGG 5084

QY 618 GACGACAGTTTACGAATCCGGTGTATCTTCTCATGACGAGTCGCAGCATTAATCGGAA 677

Db 5085 GACGACAGTTTACGAATCCGGTGTATCTTCTCATGACGAGTCGCAGCATTAATCGGAA 5144

QY 678 CTATATTCGGGTGAACCTTCTTGAACCGAATCAGCAATTTCTCGGCCAAGACCAACTCC 737

Db 5145 CTATATTCGGGTGAACCTTCTTGAACCGAATCAGCAATTTCTCGGCCAAGACCAACTCC 5204

QY 738 TCTTCAACTTGTGTAACCTCAAAACATGATAACTTGTTCCTCCCTCATACGATTAGA 797

Db 5205 TCTTCAACTTGTGTAACCTCAAAACATGATAACTTGTTCCTCCCTCATACGATTAGA 5264

QY 798 GAGAGACGAGAGAGTTCATTTTATATTAACCGCACTGTGTATTATCATAGTTTAGGTTTC 857

Db 5265 GAGAGACGAGAGAGTTCATTTTATATTAACCGCACTGTGTATTATCATAGTTTAGGTTTC 5324

QY 858 TAATAATGATAATAACAAAACCTGTGTTTCTTTCCTTCA 896

Db 5325 TAATAATGATAATAACAAAACCTGTGTTTCTTTCCTTAA 5363

RESULT 12

ATT20N10

LOCUS

DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone T20N10.

ACCESSION AL353032

VERSION AL353032.1 GI:7630060

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 90273)

D'Angelo,M., Vezzi,A., Modesto,D., Pigazzi,M., Valle,G., Mewes,H.W., Rudd,S., Lemcke,K., Mayer,K.F.X., Quetier,F. and Salanoubat,M.

Unpublished

2 (bases 1 to 90273)

EU Arabidopsis sequencing, project.

REFERENCE

AUTHORS

JOURNAL

TITLE Direct Submission

AUTHORS Submitted (19-APR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de

JOURNAL Coordinator: Marcel Salanoubat and Francis Quetier, Groupement


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/ gene="T20N10_40"
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10740..10819
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cytosolic, Arabidopsis thaliana, PIR:S49033
Contains Ribosomal protein L5 signature AA39-55"
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Query Match      37.3%; Score 334.2; DB 8; Length 90273;
Best Local Similarity 99.1%; Pred. No. 6e-81;
Matches 336; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 558 AAGATAGCCGAAGCGGCAGATTGAATCCGACAGCAGAGGAATCGAGTGTGATACAAGS 617
DB 41426 ATAGTAGCCGAGAGCGGCAGATTGAATCCGACAGCAGAGGAATCGAGTGTGATACAAGS 41485

QY 618 GACGACAGTTTACGAATCCGGTGATCTTCTCATGACCAAGTCGCGAGCATTAATCGGAA 677
DB 41486 GACGACAGTTTACGAATCCGGTGATCTTCTCATGACCAAGTCGCGAGCATTAATCGGAA 41545

QY 678 CTATATCCGGTGAACCTTCTGAACCGAATCAGCAATCTCCGGCCAGACCAACCTCC 737
DB 41546 CTATATCCGGTGAACCTTCTGAACCGAATCAGCAATCTCCGGCCAGACCAACCTCC 41605

QY 738 TCTTCAACTTGTGTAACCAACATGATACTTGTCTTCTCCCTCATACGATTAAGA 797
DB 41606 TCTTCAACTTGTGTAACCAACATGATACTTGTCTTCTCCCTCATACGATTAAGA 41665

QY 798 GAGAGCAGAGAGTTCATTTTATATTATACGGGAGTGTGATTCATAGTTAGGTTTC 857
DB 41666 GAGAGCAGAGAGTTCATTTTATATTATACGGGAGTGTGATTCATAGTTAGGTTTC 41725

QY 858 TAATAATGATATAACAACCTGTTGTTTCTTTGCTTCA 896
DB 41726 TAATAATGATATAACAACCTGTTGTTTCTTTGCTTAA 41764
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RESULT 13
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LOCUS      Malus domestica mRNA for C-type MADS box protein (mads14 gene).
DEFINITION AJ251117
ACCESSION  AJ251117.1 GI:16973295
VERSION     C-type MADS box protein; mads14 gene.
KEYWORDS    apple tree.
SOURCE      Malus x domestica
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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```

Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1
REFERENCE    1
AUTHORS      Vosman,B. and Smulders,M.J.M.
TITLE        Isolation of apple B- and C-type MADS box genes from vegetative
tissue
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 1065)
AUTHORS      van der Linden,C.G.
TITLE        Direct Submission
JOURNAL      Submitted (15-NOV-1999) van der Linden C.G., Identity and Genetic
Diversity, CPRO Wageningen University & Research Centre, PO Box 16,
Wageningen, 6700 AA, NETHERLANDS
FEATURES     Location/Qualifiers
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BASE COUNT   344 a 237 c 211 g 273 t
ORIGIN
Query Match      37.2%; Score 333.6; DB 8; Length 1065;
Best Local Similarity 69.4%; Pred. No. 6.2e-81;
Matches 491; Conservative 0; Mismatches 199; Indels 18; Gaps 2;

QY 46 AAGAAATAGGGAGAGGAGGAAATAGAGATAAGAGGATAGAGAACACACAAATCGTCAA 105
DB 179 AAAAAATTGGGAAGAGGCAAAATTGAGATTAGCGGATCGAAGAACACTACCANTCGACAA 238

QY 106 GTTACTTTCTGCAACAGCAGCAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTCTTG 165
DB 239 GTCACTTCTGCAACCGCCGACGGATTGCTTAAGAAAGCTTATGAATGTCTGTTCTT 298

QY 166 TGTGATCCGGAAGTTGCCCTCGTCACTTCTCCACTCGTGGCCGCTCTCTATGAGTACGCC 225
DB 299 TGTGATGCTGAAGTTGCTTATCGTCTCTCCACCGTGGCCGCTCTATGAGTATGCT 358

QY 226 AACACAGTGTGAGGGGTACAATTGAAAGGTACAGAAAGCTTGTTCGATGCCGCTCAAC 285
DB 359 AACACAGCGTTAGAGCAACAATCGACAGGTACAAAAAAGCATGCGCTGATTTCTACGGAC 418

QY 286 CTTCTTCCGTCACCGAGCTAAATACACTAGTACTATATCAGGAAGACCTCTAAGCTTCGG 345
DB 419 GGTGGATCTGTATCAGAAAGTAAACACTCAGTTTATCAGCAGGAAGCATATACTGGGGGA 478

QY 346 AGCAGATTTCGAGATATTTCAGAAATTCAGATATTTGTTGGGAATCACTTGCTTCC 405
DB 479 AGCAGATCCGAGAAATTCAGAAATTCAGAAAGCATATACTGGGGGAATCCCTTAGCACC 538

QY 406 TTGAACCTTCAAGGAACCTCAAAAACCTAGAGAGCGCTTTTGAAAAAGGAATCAGCGTGTTC 465
DB 539 TTGAAGTTCAGGAAGCTGAAAAACCTAGAGAGAGATTGGAGAAAGGAATCAGCAGAAATA 598

QY 466 CGCTCCAAAAGAGATGAGCTGTTAGTGCAGAGATAGAGTATATCAGAGAGAGGAAATG 525
DB 599 AGATCCAAAAGAGATGAATCCTGTTTCTGAAATTCGAATTCATGCAAAAGAGGAGACT 658

QY 526 GAGTTGCAACAACAATAACATGTACTCGGAGCAAAAGATAGCCGAAGGCCCGCCAGATTGAAT 585
DB 659 GAGCTGCAACACCACCAACAATTTCTGAGAGCAAAAGATAGCTGAAAGCGGAGAG--GGAA 715
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QY	586	CCGGACAGCAGCAATCGAGTGTGATACAAGAGGACAGCATTTACGAATCCGGTGTAATCT	645
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Db	821	AATAACCAATTTACCTCGCCCAAGCCAGACAGCTCTCCAATCTTGTGA 868	
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LOCUS			
DEFINITION	P.hydrida pMADS3 mRNA..	1214 bp	mRNA linear PLN 15-NOV-1993
ACCESSION	X72912		
VERSION	X72912.1	GI:313112	
KEYWORDS	homeotic flower gene; MADS box; pMADS3 gene; transcriptional regulation.		
SOURCE	Petunia x hybrida.		
ORGANISM	Petunia x hybrida.		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.		
AUTHORS	1 (bases 1 to 1214)		
TITLE	Tsuchimoto,S., van der Krol,A.R. and Chua,N.H.		
JOURNAL	Ectopic expression of pMADS3 in transgenic petunia phenocopies the		
MEDLINE	Petunia blind mutant		
PUBMED	Plant Cell 5 (8), 843-853 (1993)		
REFERENCE	94004017		
AUTHORS	2 (bases 1 to 1214)		
TITLE	Tsuchimoto,S.		
JOURNAL	Direct Submission		
MEDLINE	Submitted (26-MAR-1993) S. Tsuchimoto, The Rockefeller University,		
PUBMED	1230 York Ave., New York, NY 10021, USA		
REFERENCE	Location/Qualifiers		
AUTHORS	1. .1214		
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MEDLINE	YLOVNGIQTNHNHPRODQPPLQLV		
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Db 197 AAAATGGGAAGAGGAGATCGAAATTAAGCGGATCGAGAGACACCACTAATCGACAAGTC 256
Qy 109 ACTTCTGCAACAGCAGCAATGGTCTCTCAAGAAAGCTTATGAACCTCTCTCTTGTGT 168
Db 257 ACCCTCTGTAGCGCCGCAACGGCTTGCTCAAAAAGGCTATGAATTATCGGCTTATGT 316
Qy 169 GATGCCGAAGTTGGCCTCGTCATCTTCCACTCGTCGCCGCTCTCTATGAGTACGCCAAC 228
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Qy 409 AACTTCAAGGAACCTCAAAAACCTAGAGGACGCTTGTGAAAAAGGAATCAGCCGTGTCCGC 468
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Qy 589 GACCAGCAGGAATCGAGTGTATACAAAGGACGACAGTTTACGAATCCGGTGTATCTTCT 648
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Db 833 CACCATTACTCTCGGCCACGACCAACAGCTCTCCAACTAGTGTGA 877
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 08:21:19 ; Search time 1738.09 Seconds
(without alignments)
8935.939 Million cell updates/sec

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Perfect score: 959
Sequence: 1 gaattcatcttccatctc.....ccaagagacggttacacaa 959

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	451	47.0	615	10	AV557878
C 2	397	41.4	452	9	AU227814
C 3	385	40.1	537	10	AV556852
4	331.4	34.6	686	14	BQ411600
5	329.8	34.4	656	14	BQ411583
6	328.4	34.2	748	13	BI311095

7	318.4	33.2	754	13	BI310910
8	316.2	33.0	636	14	BQ123247
9	308	32.1	624	10	AW277843
10	304.6	31.8	555	13	BI272847
11	301.6	31.4	548	10	AW277299
12	298.8	31.2	656	10	BE659918
13	292.4	30.5	776	12	BG445079
14	292.4	30.5	866	12	BG441292
15	292.4	30.5	892	12	BG444639
16	292.2	30.5	715	13	BI933168
17	290	30.2	848	12	BG445047
18	288.6	30.1	642	9	AI725968
19	285.6	29.8	597	9	AI729115
20	285	29.7	632	10	AW185524
21	279.8	29.2	754	9	AI731375
22	279.8	29.2	761	9	AI731368
23	279.6	29.2	649	10	AW184799
24	278.8	29.1	548	10	BE434089
25	278	29.0	607	10	AW705451
26	276.2	28.8	538	10	BE433121
27	274.4	28.6	562	9	AI727662
28	274	28.6	698	10	BE659915
29	271.8	28.3	597	10	AW704750
30	271.4	28.3	608	10	AW278878
31	269	28.1	566	9	AI728519
32	267	27.8	754	13	BI311053
33	266.4	27.8	960	12	BG445265
34	261.4	27.3	802	13	BI925669
35	260.2	27.1	539	9	AI771796
36	259.4	27.0	584	12	BG442607
37	259.2	27.0	885	14	BQ796770
38	257.4	26.8	600	9	AI728967
39	256.2	26.7	586	12	BG446848
40	255.6	26.7	537	9	AI486290
41	255	26.6	558	10	AW705789
42	255	26.6	613	10	BE659913
43	254.8	26.6	929	12	BG444491
44	251.4	26.2	498	12	BF112843
45	249	26.0	892	12	BG415259

ALIGNMENTS

RESULT 1	AV557878/c	AV557878	615 bp	mrna	linear	EST 07-SEP-2000
LOCUS	AV557878	Arabidopsis thaliana	green siliques	Columbia	Arabidopsis	
DEFINITION	thaliana	cdna clone SQ083b07F 3',	mrna	sequence.		
ACCESSION	AV557878					
VERSION	AV557878.1	GI:8729293				
KEYWORDS	EST.					
SOURCE	Arabidopsis thaliana					
ORGANISM	thale cress.					
REFERENCE	Arabidopsis thaliana					
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
TITLE	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi					
	1 (bases 1 to 615)					
	Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.					
	A large scale analysis of cDNA in Arabidopsis thaliana: Generation					
	of 12,028 non-redundant expressed sequence tags from normalized and					
	size-selected cDNA libraries					
JOURNAL	DNA Res. 7, 175-180 (2000)					
MEDLINE	20363093					
COMMENT	Contact: Erika Asamizu					
	The First Laboratory for Plant Gene Research					
	Kazusa DNA Research Institute					
	Yana 1532-3, Kisarazu, Chiba 292-0812, Japan					
FEATURES	Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.					
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Best Local Similarity 100.0%; Pred. No. 7.9e-123;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 711 TCTTCTCACAGTCGGGCGAGTATAACCGGAATATATGCGGTTAACTTCTTGAACCG 770
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QY 831 TAAGTCTCTTTCTCAGCCTGAGATCGATCT 861
Db 195 TAAGTCTCTTTCTCAGCCTGAGATCGATCT 165

RESULT 2
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LOCUS           AU227814 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-25-E19 3',
DEFINITION      mRNA sequence.
ACCESSION       AU227814.1 GI:19742461
VERSION         AU227814.1
KEYWORDS        EST.
SOURCE          Arabidopsis thaliana
ORGANISM        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                1 (bases 1 to 452)
                Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
                Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
                Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu
                M., Hayashizaki,Y. and Shinozaki,K.
                Large scale analysis of Arabidopsis full-length cDNA
                Unpublished (2002)
                Contact: Motoaki Seki
                Plant Functional Genomics Research Group
                RIKEN Genomic Sciences Center
                3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                Tel: 81-298-36-4359
                Fax: 81-298-36-9060
                Email: mseki@rtc.riken.go.jp

REFERENCE
AUTHORS         Contact: Erika Asamizu
```

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

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Matches 413; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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RESULT 3
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LOCUS           AV556852 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION      thaliana cDNA clone SQ053h11F 3', mRNA sequence.
ACCESSION       AV556852
VERSION         AV556852.1
KEYWORDS        EST.
SOURCE          thale cress.
ORGANISM        Arabidopsis thaliana
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                1 (bases 1 to 537)
                Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
                A large scale analysis of cDNA in Arabidopsis thaliana: Generation
                of 12,028 non-redundant expressed sequence tags from normalized and
                size-selected cDNA libraries
                DNA Res. 7, 175-180 (2000)
                20363093
                Contact: Erika Asamizu
```

The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Kazusa 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

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 DEFINITION
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 arboreum cDNA clone GA_Ed0041B08f, mRNA sequence.

ACCESSION BQ411600
 VERSION BQ411600.1 GI:21099287
 KEYWORDS EST.
 SOURCE
 ORGANISM
 Gossypium arboreum.
 Gossypium arboreum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

REFERENCE
 AUTHORS
 1 (bases 1 to 866)
 Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
 D., Wood,T.C., Leslie,A. and Wilkins,T.A.
 An integrated analysis of the genetics, development, and evolution
 of the cotton fiber

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clcmson.edu
 Total High Quality bases = 612
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 Db 177 TGTGATGCTGAGGTGCTCTCATAGTCTTCTCCAGCGCTGCGCGTCTCTATGAATATGCT 236
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 QY 297 AACACAGTGTGAGAGGAACAATAGAAAGGTACAAAGAAAGCTTGTCTCCGACCGCTTAAC 356
 |||||
 Db 237 AACACAGTGTGAGAGGAACAATAGAAAGGTACAAAGAAAGCTTGTCTAGATGCAACAAC 296
 |||||
 QY 357 CCTCCGACCATCACCGAAGCTAATCTACGTACTTATCAGCAAGAGCGCTCTAAACCTCCGG 416
 |||||
 Db 297 CCAGGCTGTGGCTGAAGCCATTATTCAGTTTACAGCAAGAGCAACCAACTCCGA 356
 |||||
 QY 417 AGACAGATTCGGGACATTCAGAAATTTGAACAGACACATTTCTTGTGTAATCTCTTGGTTCC 476
 |||||
 Db 357 CGACAAATTCGTGATGTTCAAGACATGAACAGGCGATATCTTTGGAGAGGCTCTGAGCTCA 416
 |||||
 QY 477 TTGAACCTTTAAGGAACCTCAAGAACCTTGAAGTAGGCTTGAGAAAGCAATCAGTCGTGTC 536
 |||||
 Db 417 TTGAACCTTTAAGGAACCTCAAGAACCTTGAAGTAGGCTTGAGAAAGCAATCAGTCGTGTC 476
 |||||
 QY 537 CGATCCAAAGAACGACGAGATGTTAGTTCGAGAGATTGAATACATGCAAAAAAGGGAATC 596
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 Db 477 AGATCCAAAGAACGACGATTTACTGTTGCAAAATTTGGATTTCGAAAGAGGGAAGTT 536
 |||||
 QY 597 GAGTCGCAAAAGGATAACATGATATCTCCGCTCCAAGATTACTGAAAGACAGGCTACAG 656
 |||||
 Db 537 GAATTCGCAAGACGATAACATGATACCTCGAGCAAAAATAGCTGAAATGAAAGAGCGCAA 596
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 QY 657 CAACAAGATCCAGTGTGATACATCAAGGACAGTTTACGA 697
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 Db 597 CAACAATCAACACGCTGTATACAAAGCAGCGCTCTCTCTACAA 637
 |||||

RESULT 5
 BQ411583 656 bp mRNA linear EST 22-MAY-2002
 LOCUS
 DEFINITION
 GA_Ed0041A08f Gossypium arboreum 7-10 dpa fiber library Gossypium
 arboreum cDNA clone GA_Ed0041A08f, mRNA sequence.
 ACCESSION BQ411583


```
Db 83 AAGAAATGGGAAGAGGAAAAATGAAATCAAGAGGATTGAAACACTACCAATAGGCAA 142
Qy 177 GTCACCTTCTGCAAGCGCATGCTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTTG 236
Db 143 GTCACCTTTTGCAGAGCGCAATGATGTTGTTGAAGAAAGCTTATGAATATCCGTTCTT 202
Qy 237 TGTGACGCTGAGTGTCTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 296
Db 203 TGTGATGCGGAAGTTGCTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 262
Qy 297 AACACAGTGTGAGAGGACAAATAGAAAGGTGAGAAAGCTTGTCTCCGACGCGTTAAC 356
Db 263 AACACAGTGTGAGAGGACAAATAGAAAGGTGAGAAAGCTTGTCTCTCTCTCTCTCTCT 322
Qy 357 CCTCGACCATCACCGAGCTAATCTACTACTACTACTACTACTACTACTACTACTACTACT 416
Db 323 GCAGATCTGTATCTGAGAGCTAATACCCAGTTTACCGCAAGAAATCATCCAAATGAGA 382
Qy 417 AGACAGATTCGGGACATTCAGAAATTTGAACAGACACATTTCTTGGTGAATCTCTTGGTTC 476
Db 383 AGACAGATTCGAGATATTGAGAAATCTAAATAGACACATCTTGGTGAAGCTCTAGGATCT 442
Qy 477 TTGAACCTTAAAGGAATCAAGAACTTGAAGAGCTTGAAGAGGATTCAGTCGCTGTCT 536
Db 443 CTAAGTCTCAAGAACTGAAGAACTTGAAGAGGATGAGAGGATGAGAGGATTTAAGCAGAGTT 502
Qy 537 CGATCCAAAGAGCAGCAGATGTTAGTTGAGAGATTTGATACATGCAAAAGGAAATC 596
Db 503 AGATCTAAGAGCATGAGACTTTGTTGCTGATGTGGAGTTTCATGCAAAAGCGGAAAT 562
Qy 597 GAGTGTCAAAAGCATATCATGCTCCGCTCCAGATTTACTGAAAGAACAGGCTCTACAG 656
Db 563 GAGTGTCAAAAGCATATCAAAATTTACTACGGCTAAGATAGCGGAACATGAGAGGCTCAA 622
Qy 657 CAACAAGAACTGAGTGTATCATATCAAGGACAGTTTACGAGTCGGGTGTATCTCTCT 716
Db 623 CAACGCAACATATTTGATGCGCATCAAAACAAATGTGTGATCAGTCCTTACCTTCATCA 682
Qy 717 CACAGTGGGGCAGTATACCGGAATATATTTGGGGTTAACTTCTTGAACCGAATCAG 776
Db 683 CA-----AGCATATGACCGAAATTTCTTCCGGTAAATCTCTTGGATCAGATCAG 733
Qy 777 AA 778
Db 734 CA 735

RESULT 7
BI310910
LOCUS
DEFINITION
BI310910 754 bp mRNA linear EST 20-JUL-2001
ACCESSION
BI310910 mRNA sequence.
VERSION
BI310910.1 GI:14985237
KEYWORDS
EST.
SOURCE
barrel medic.
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 754)
Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho
, J. and Fraser, C.M.
ESTs from developing reproductive tissues of Medicago truncatula
Unpublished (2001)
Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
Fax: 713-798-7078
Email: mgrusak@bcm.tmc.edu
```

B397765e

TIGR sequence name: MTPAN717K
More information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

FEATURES

Source

1..754

/organism="Medicago truncatula"

/cultivar="A17"

/db_xref="taxon:3880"

/clone_lib="pGESD9K22"

/clone_lib="GESD"

/tissue_type="immature seeds"

/dev_stage="Immature seeds, 11 to 19 days after

pollination"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Immature seeds, collected from pods ranging in age from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XIOLR cells."

BASE COUNT 245 a 144 c 159 g 206 t

ORIGIN

Query Match 33.2%; Score 318.4; DB 13; Length 754;

Best Local Similarity 68.9%; Pred. No. 2.1e-83;

Matches 471; Conservative 0; Mismatches 201; Indels 12; Gaps 2;

Qy 139 TAGAGATAAGAGGATAGAGACACTACGAATCGTCAAGTCACCTTCTGCAAAACGCGCA 198

Db 1 TTGAATCAAGAGGATTGAAACACATACCAATAGCGAAGTCACCTTTGCAAAACGCGCA 60

Qy 199 ATGGTTTACTCAAGAGCTTATGAGCTCTCTGCTTGTGTGAGCGCTGAGGTTGCTCTTG 258

Db 61 ATGGGATGTTGAGAAAGCTTATGAATATTCGTTCTTGTGATGCCGAAGTTGCTCTTG 120

Qy 259 TCATCTTCTCCACTCGAGGCGGCTCTACGAGTACGCCAACCAACAGTGTGAGAGCAACA 318

Db 121 TTGCTCTTCCACTCGCGGCTGTTGTATGATGATGCCAACAGAGTGTAGAGCAACTA 180

Qy 319 TAGAAAGGTACAGAAAGCTTGTCTCCGACCGGTTAACCTCCGACCATCACCGAAGCTA 378

Db 181 TTGAAAGGTACAGAAAGCTTGTCTCCACTAACGCGAGAATCTGTATCTGAAGCTA 240

Qy 379 ATACTCAGTACTATCAGCAAGAGCGCTCTAACTCCGGACACAGATTCGGGACATTCAGA 438

Db 241 ATACCCAGTTTACCAGCAAGAAATCATCCAAATTTGAGAAAGCAGATTGAGATATTCAGA 300

Qy 439 ATTTGAACAGACACACTTCTTGGTGAATCTCTTGGTCTCTTGAACCTTTAAGAACTCAAGA 498

Db 301 ATCTAAATAGACACATCTTGGTGAAGCTAGATCTCTAAGTCTCAAGAACTGAAGA 360

Qy 499 ACCTTGAAGTAGGCTTGAAGAAAGAAATCAGTCGTGTCGATCCAAAGAACGACGATGT 558

Db 361 ATCTTGGAGGTAGATTGGAGAAAGGTTTAAAGCAGAGTTAGATCTAGAAAGCATGAGACTT 420

Qy 559 TAGTTGCAGAGATTGAATCATGCAAAAGGAAATCGAGCTGCAAAACCATACATGT 618

Db 421 TGTTCGTGATGAGGTTTCGCAAAAGCGGAAATTTAGCTGCAAAACCATACCAAT 480

Qy 619 ATCTCCGCTCCAAGATTACTGAAAGAAACAGGCTACAGCAACAGAAATTCGAGTGTGATAC 678

Db 481 ATCTACGGGCTAAGATAGCGGACATGAGAGAGCTCAACAGCAGCAACATATTTGATGC 540

Qy 679 ATCAAGGGACAGTTTACGAGTCGGGTGTTTACTTCTTCTACCAAGTCGGGGCAGTATACC 738

Db 541 CAGATCAAAACAAATGTGTATCAGTCCTTACCTTCATCACA-----ACCATATGACC 591

QY	739	GGAAATATATGCGGTAACTCTCTTGAACCGAAT---	CAGAAATTCCTCCAAACCAAGACC	795
Db	592	GAATTTCTTCCGGTAAATCTTCTTGGATCAGATCAGCAGCAGTATTCGGTCAAGACC	651	
QY	796	AACCACTCTGCAACTTGTGTGAT	819	
Db	652	AAATGCGCCTCCACTTGTGTGAT	675	

RESULT 8	
BQ123247	
LOCUS	636 bp mRNA linear EST 17-APR-2002
DEFINITION	EST060823 GLSD Medicago truncatula cDNA clone pGLSD-31F11, mRNA sequence.
ACCESSION	BQ123247
VERSION	BQ123247.1 GI:20175209
KEYWORDS	EST.
SOURCE	barrel medic.
ORGANISM	Medicago truncatula
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE	1 (bases 1 to 636)
AUTHORS	Grusak, M.A., Samac, D., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
TITLE	ESTs from late stage developing seeds of Medicago truncatula
COMMENT	Unpublished (2002) Contact: Grusak, M.A. USDA/ARS Children's Nutrition Research Center Baylor College of Medicine 1100 Bates Street, Houston, TX 77030-2600, USA Tel: 713 798 7044 Fax: 713 798 7078 Email: mgrusak@bcm.tmc.edu TIGR sequence name: MTRAO30TK More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gTg gAT CC).

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FEATURES             Location/Qualifiers
     1..636
     /organism="Medicago truncatula"
     /cultivar="A17"
     /db_xref="taxon:3880"
     /clone="pGLSD-31r11"
     /clone_lib="GLSD"
     /tissue_type="Immature seeds"
     /dev_stage="25 to 35 days after pollination"
     /lab_host="XL0LR"
     /note="vector: pluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Immature seeds, collected from pods ranging in age
from 25 to 35 days after pollination, were harvested from
greenhouse-grown plants. Seed were removed and separated
from pod walls and immediately frozen in liquid nitrogen.
Seeds throughout the age range were pooled for mRNA
extraction. cDNA was prepared from polyA+ enriched RNA.
The cDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Gigapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in XL0LR cells."

BASE COUNT          215 a 115 c 136 g 170 t
ORIGIN
Query Match          33.0%; Score 316.2; DB 14; Length 636;
Best Local Similarity 69.5%; Pred. No. 9.2e-83;
Matches 448; Conservative 0; Mismatches 188; Indels 9; Gaps 1;

Qy 123 ATAGGGAGGAGATAGATTAAGAGGATAGAGACACTACGACATCGTCAAGTCACT 182
      ||| ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1 ATGGGAGGAGGAAAAATGAAATCAAGAGGATGTGTAACACTTACCANTAGGCAAGTCACT 60
      ||| ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Ov 183 TTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTGTCTGTGTGAC 242

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[illegible]

RESULT	9
AUW77843	
LOCUS	sF87d01.y1 Gm-cl019 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION	Gm-cl019-3098 5' similar to SW:AGLS_ARATH P29385 FLORAL HOMEOTIC PROTEIN AGL5., mRNA sequence.
ACCESSION	AUW77843
VERSION	AUW77843.1 GI:6666384
KEYWORDS	EST.
SOURCE / ORGANISM	Glycine max Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine. 1 (bases 1 to 624) Shoenmaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvelli,V., Khanna, .A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin.J., Beck,C., Wylie.T., Underwood,K., Stepcoe.M., Theising.B., Allen.M., Bowers .Y., Person,B., Swaller,T., Gibbons.M., Pope.D., Harvey.N., Schurk .R., Ritter.E., Kohn.S., Shin,T., Jackson.Y., Cardenas.M., McCann .R., Waterston.R. and Wilson.R. Public Soybean EST Project Unpublished (1999)
JOURNAL	Contact: Shoemaker R/Public Soybean EST Project
COMMENT	Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1024 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 446.

FEATURES

source
Location/Qualifiers
1. .624
/organism="glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1019-3098"
/clone_lib="Gm-c1019"
/tissue_type="immature seed coats of greenhouse grown plants"
/lab_host="DH10B (Gibco BRL)"
/note="Vector: pSPORT1 (Life Technologies); Site 1: Not I; Site 2: Sal I; This cDNA library was constructed from mRNA isolated from immature seed coats (200-300 mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E. coli Electromax DH10B host cells (Gibco BRL). This library was constructed by Dr. Lilia Vodkin and Dr. Anu Khanna."
210 a 124 c 145 g 142 t 3 others

BASE COUNT

ORIGIN
Query Match 32.1%; Score 308; DB 10; Length 624;
Best Local Similarity 69.0%; Pred. No. 2.5e-80;
Matches 419; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

Qy 68 GCTTATAGAAATGGAGGTGGTGGCGAGTAAATGAAGTAGCAGAGCAGCAGCAAGAGATAGG 127

Db 18 GCTTCCCAACCATGGAGATCCAAATCAAGCTCCAGAAGCGCTCTCTCAGAGAAGAAATGGG 77

Qy 128 GACGGGAGATAGAGATAAAGAGGTAGACACATACCAATCGTCAAGTCACTTCTCTG 187

Db 78 AAGAGGAAGATTGAATCAACGGATCGAGAACACCAATAGGCAATGAGCAATCACTTCTG 137

Qy 188 CAACGACCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGTGACGCTGA 247

Db 138 CAACGCGCCCAACGGTTTCTGCTGAAAAAGCTTATGAATATCATGTTCTGTGTGATGCTGA 197

Qy 248 GTTGTCTTTGTCATCTTCTCCACTCAGCCGCTCTCTAGAGTACGCCAACACAGTGT 307

Db 198 AGTTGCCCTTGTGTCTTCTCAACCGCTGGCCGTTTGTATGAGTATGCCAACACAGTGT 257

Qy 308 GAGGGAACAATAGAAAGGTACAGAAAGCTTGCTCCGACGCGTTAAACCTCCGACCAT 367

Db 258 TAGGCCACATATTGAGGTTACAGAGGCAAAATGCTGTCTTCAACGCAAGATCCGT 317

Qy 368 CACCGAAGCTAATACGTACGTATCAGCAAGAGCGGTCTAAACTCCGGAGACAGATTCG 427

Db 318 ATCTGAAGCTAACACACAGTCTTACCAGCAAGAGTATCCAAAATTTGAGAAGACAATTCG 377

Qy 428 GCACATTCAGATTTTCAACAGACACATCTTGTGTAATCTCTTGGTTCCTTGAACCTTAA 487

Db 378 AGATATTCAGATCTTAACAGGACATCTTGTGTGAAGCACTTGGTCTCTGAGTCTCAA 437

Qy 488 GGAACCTCAAGAACCTTGAAGTAGTGGCTTGAGAAAGGAATCAGTCTGCCGATCCCAAGAA 547

Db 438 GGAACCTAAAGAACCTCGAGGCTAGATTGGAGAAGGATTAAGCAGAGTTAGATCTAGAAA 497

Qy 548 GCACAGATGTTAGTTGCGAGAGATTGAATACATGCCAAAAGGGAATCGAGCTGCAGAAA 607

Db 498 GCATGANACATTTGTTGCTGATGTGAGTTTCATGCAANAACGGGAAATGAGCTGCANAA 557

Qy 608 CGATACATGTATCTCCGCTCCCAAGATTACTGAAAGAAACAGGTCTACAGCAACCAAGAAAT 667

Db 558 CCACACAAATTTATCTCGAGCTAAGATAGCTGACATGAGAGAGCTCAACACAGCAATC 617

Qy 668 GAGTGTG 674

Db 618 AAATATG 624

RESULT 10

Bi272847

LOCUS

DEFINITION

NC097609FL1071 Developing flower

Medicago truncatula cDNA clone

555 bp mRNA linear EST 18-JUL-2001

NC097609FL 5', mRNA sequence.

ACCESSION

Bi272847

VERSION

Bi272847.1

KEYWORDS

EST.

SOURCE

barrel medic.

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

REFERENCE

1 (bases 1 to 555)

AUTHORS

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,

Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

TITLE

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula flower library

JOURNAL

Unpublished (2001)

COMMENT

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7391

Fax: 580 221 7380

Email: gmay@noble.org

Insert Length: 555 Std Error: 0.00

Plate: 097 row: G column: 09

Seq primer: TCACACAGCAACAGCTATGAC.

FEATURES

Location/Qualifiers

1. .555

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF097G09FL"

/clone_lib="Developing flower"

/tissue_type="Developing flowers"

/dev_stage="Developmentally pooled. Contains a mixture of

very young, developing, fully-opened flowers and flowers

in early transition into pods."

/note="Vector: Lambda Zap: cDNA was prepared from polyA+

enriched, pooled samples of equivalent amounts of total

RNA from very young, developing, fully-opened flowers and

flowers transitioning into pods. The cDNA was

directionally ligated into the Uni-Zap XR vector

(Stratagene) and packaged using the Gigapack III Gold

packaging extracts. Phagemids containing cDNA inserts were

in vivo excised from the recombinant Uni-Zap XR vector

using EXAssist helper phage and the E. coli strain

XLI-Blue MRF' (Stratagene). Excised plasmids were plated

using SOLR cells."

BASE COUNT 194 a 120 g 143 t 6 others

ORIGIN

Query Match 31.8%; Score 304.6; DB 13; Length 555;

Best Local Similarity 74.5%; Pred. No. 2.5e-79;

Matches 379; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

Qy 117 AAGAAGATAGGGAGAGGGAAGATAGAGATAAGAGATAGAGAACACTAGCAATCGTCAA 176

Db 45 AGAAAATGGGAGAGAGAAAATTTGAATCAAGAGGATTGAACACTACCAATAGCAAA 104

Qy 177 GTCACTTTTGTGCAACAGCGCAATGTTTACTCAAGAAAGCTTATGAGCTCTCTGTTTG 236

Db 105 GTCACTTTTGTGCAACAGCGCAATGTTTACTCAAGAAAGCTTATGAGCTCTCTGTTTG 164

Qy 237 TGTGACGCTGAGGTGCTCTTGTTCATCTTCCACTCGAGCGCTCTCTACGAGTACGCC 296

QY	297	AAACAACAGCTGTGAGAGAACATATAGAAAGCTTACAGAAAGCTTGCCTCCGAGCGCGTTAAC	356
Db	285	AAACAACAATAAGATCAACAATAGACAGCTAGCAAGAAGCTTGCCTCAGATACCTTCTTAAC	344
QY	357	CTCCGACCATCACCGAAGCTAATACTACGTACTATCAGCAAGAGGGCTCTAAACTCCGG	416
Db	345	ACAAACACTGTTACTGAAATCAATGCTCAGTATATCAACAAGNATCAGCAAGTTGAGA	404
QY	417	AGACAGATTCCGGGACATTCAGAAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCC	476
Db	405	CAGCAGATTCAAAATGTACAGAATCTTAACAGGCACCTAATGGAGAGATTCTTGGAGTTCC	464
QY	477	TTGAACCTTAAAGAACTCAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTC	536
Db	465	TTAACTGTGAAAGAGTTAAAGCAGGTAGAAACAGGCTTGAAGAGGAATTAAGTAGATC	524
QY	537	CGATCCAAAGAACGACGAGATGTTAGTTGCGAGAGATTGAATACATGCAAAAAGGAAATC	596
Db	525	AGGTCCAAGAACGAGAAATGCTACTAGCTGAAATAGAGTTTTTTCGACAAAAGGAAATC	584
QY	597	GAGTGTGAAAAACGATACATGTATCTCCGCTCCAGATTTACTGAAAGACACAGGTTACAG	656
Db	585	GAATTGGAATAAGAAAGTGTGTCTCCGACCAAGATTGCAGAAATTGAGAGGCTTCAG	644
QY	657	CA 658	
Db	645	CA 646	
RESULT 14			
LOCUS	BG441292		
DEFINITION	BG441292 866 bp mRNA linear EST 15-MAR-2001 arborescens cDNA clone GA_Ea0012J14f, mRNA sequence.		
ACCESSION	BG441292		
VERSION	1		
KEYWORDS	GI:13350932		
SOURCE	Gossypium arboreum.		
ORGANISM	Gossypium arboreum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.		
AUTHORS	Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry D., Wood, T.C., Leslie, A. and Wilkins, T.A.		
TITLE	An integrated analysis of the genetics, development, and evolution of the cotton fiber		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: TAATACGACCTACTATAGGG High quality sequence stop: 676. Location/Qualifiers 1. 866 /organism="Gossypium arboreum" /strain="AKA" /cultivar="8400" /db_xref="taxon:29729" /clone="GA_Ea0012J14f" /clone_lib="Gossypium arboreum 7-10 dpa fiber library" /tissue_type="Fibers isolated from bolls harvested 7-10 dpa" /lab_host="E. coli" /note="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"		
FEATURES	source		
BASE COUNT	297 a	158 c	188 g
ORIGIN	297 a 158 c 188 g 218 t 5 others		
Query Match	30.5%; Score 292.4; DB 12; Length 866;		

[illegible]

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FEATURES                               Location/Qualifiers
Source                                1..892
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0025A08f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT      303 a      161 c      192 g      223 t      13 others
ORIGIN

Query Match      30.5%; Score 292.4; DB 12; Length 892;
Best Local Similarity 71.2%; Pred. No. 1.2e-75;
Matches 386; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 117 AGAAGATAGGGAGAGGAAGATAGAGATAAGAGAGTAGAGAACACTACGAATCGTCAA 176
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 89 AGAGAATGGGAAGAGAAAATAGATAAGAGAGGATCGAAAACACAAATCGTCAG 148

QY 177 GTCACCTTCTGCAAGACCAATGTTACTCAAGAAAGCTTATGAGCTCTCTCTTG 236
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 149 GTTACCTTTTGCAAACCGAGAAATGGCTGCTGAAGAAAGCTTACGAACCTGTCAGTCTG 208

QY 237 TGTGACGCTGAGCTTGCTTGCTCATCTTCTCCACTCGAGGCCGCTCTCTACGAGTACGCC 296
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 209 TGTGATGCTGAAGTTGCTCTCATTTGCTTCTCCAGTCGAGGCCGCTCTGTATGAGTACTCC 268

QY 297 AACACAGTGTGAGAGGAACAATAGAAAGGTACAAAGAGCTTGCTCGGAGCCGTTAAC 356
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 269 AACACAACATAAGATCAACAATAGACAGGTACAAAGAGGCTTGCTCAGATACACTTCTAAC 328

QY 357 CTTCCGACCATCACCGAAGCTAATACACTACGTACTATCAGCAAGAGGGCTCTAAACTCCGG 416
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 329 ACAACACTGTTACTGAATCAATGCTCAGTATTATCAACAAGATCAGCCAGTTGAGA 388

QY 417 AGACAGATTCGGGACATTCAGATTTGAAACAGACACATTCCTTGGTGAATCTCTTGGTTCC 476
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GenCore version 5.1.3
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(without alignments)
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Title: US-09-978-382A-5

Perfect score: 959

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	959	100.0	959	9	US-09-981-087A-5
3	959	100.0	959	9	US-09-978-382A-5
4	959	100.0	959	9	US-09-978-740A-5
5	959	100.0	959	10	US-09-978-730-5
6	536.8	56.0	896	9	US-09-978-729A-3
7	536.8	56.0	896	9	US-09-981-087A-3
8	536.8	56.0	896	9	US-09-978-382A-3
9	536.8	56.0	896	9	US-09-978-740A-3
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21	138.2	14.4	666	9	US-09-938-842A-2442	Sequence 2442, Ap
22	132.8	13.8	753	9	US-09-853-450-29	Sequence 29, Appl
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24	126.6	13.2	747	9	US-09-853-450-27	Sequence 27, Appli
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26	124.4	13.0	705	9	US-09-938-842A-2404	Sequence 2404, Ap
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45	91.2	9.5	365	10	US-09-878-574-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1

US-09-978-729A-5

; Sequence 5, Application US/09978729A

; Patent No. US20020178465A1

; GENERAL INFORMATION:

; APPLICANT: Vanofsky, Martin F.

; APPLICANT: Liljegren, Sarah

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 19452A-000950US

; CURRENT APPLICATION NUMBER: US/09/978,729A

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: US 60/090,649

; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: US 09/339,998

; PRIOR FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 959

; TYPE: DNA

; ORGANISM: Arabidopsis sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (78)..(818)

; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)

US-09-978-729A-5

Query Match 100.0%; Score 959; DB 9; Length 959;
Best Local Similarity 100.0%; Pred. No. 2.3e-292;
Matches 959; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 5, Application US/09981087A
; Patent No. US20020178456A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: Farrandiz, Cristina
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-0009400S
; CURRENT APPLICATION NUMBER: US/09/981,087A
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998

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; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
US-09-981-087A-5

Query Match 100.0%; Score 959; DB 9; Length 959;
Best Local Similarity 100.0%; Pred. No. 2,3e-292;
Matches 959; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20020194647A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-0009300S
; CURRENT APPLICATION NUMBER: US/09/978,382A
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
US-09-978-382A-5

Query Match 100.0%; Score 959; DB 9; Length 959;
Best Local Similarity 100.0%; Pred. No. 2.3e-292;
Matches 959; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-978-740A-5
; Sequence 5, Application US/09978740A
; Publication No. US20030005481A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-0009600S
; CURRENT APPLICATION NUMBER: US/09/978,740A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(818)
; OTHER INFORMATION: AGAMOUS-LIKE 5 (AGL5)
US-09-978-740A-5

Query Match 100.0%; Score 959; DB 9; Length 959;
Best Local Similarity 100.0%; Pred. No. 2.3e-292;
Matches 959; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATCTTCCCATCTCACTCTCTTTCTTCTTGATCATATAATTAATCTGTAAGCC 60
|||||
Db 1 GAATTCATCTTCCCATCTCACTCTCTTTCTTCTTGATCATATAATTAATCTGTAAGCC 60
QY 61 AGCTAGGCTTTATAGAAATGGAGGTGGTGCAGTAATAGAGTAGCAGAGCAGCAAGA 120
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RESULT 6
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; Sequence 3, Application US/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978,729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
US-09-978-729A-3
Query Match 56.0%; Score 536.8; DB 9; Length 896;
Best Local Similarity 82.1%; Pred. No. 3.4e-159;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;
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; Sequence 3, Application US/09981087A
; Patent No. US20020178466A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: Farrandiz, Cristina
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000940US
; CURRENT APPLICATION NUMBER: US/09/981,087A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
US-09-981-087A-3
Query Match 56.0%; Score 536.8; DB 9; Length 896;
Best Local Similarity 82.1%; Pred. No. 3.4e-159;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;
Qy 77 AATGGAGGGTGGTGGAGTAATGAGTACGAGAGCAGCAAGAAGATAGGGAGAGGAA 136
Db 6 AATGGAGGAAGTGGGAGTAGTCACGACGAGAGTAGCAAGAAGTACGAGAGAGGAA 65
Qy 137 GATAGATAAAGAGGATAGAGACACTAGCAATCGTCAAGTCACTTTCTGCAAAACGACG 196
Db 66 AATGAGATAAAGAGGATAGAGACACTAGCAATCGTCAAGTCACTTTCTGCAAAACGACG 125
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Qy 257 TGTCACTTCTCCACTCGAGGCCGCTCTACGAGTACGCCAACCAACAGTGTGAGAGAAC 316
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Qy 497 GAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGCTCCGATCCAAAGACGACGAGAT 556

Query Match	56.0%	Score 536.8	DB 9	Length 896
Best Local Similarity	82.1%	Pred. No. 3.4e-159		
Matches 632	Conservative 0	Mismatches 132	Indels 6	Gaps 1
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LOCATION: (7)..(753)				
OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)				
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; TITLE OF INVENTION: Plants									
; FILE REFERENCE: 19452A-000920US									
; CURRENT APPLICATION NUMBER: US/09/978.730									
; CURRENT FILING DATE: 2001-10-15									
; PRIOR APPLICATION NUMBER: US 60/090,649									
; PRIOR FILING DATE: 1998-06-25									
; PRIOR APPLICATION NUMBER: US 09/339,998									
; PRIOR FILING DATE: 1999-06-25									
; NUMBER OF SEQ ID NOS: 25									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 3									
; LENGTH: 896									
; TYPE: DNA									
; ORGANISM: Arabidopsis sp.									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (7)..(753)									
; OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)									
US-09-978-730-3									
Query Match 56.0%; Score 536.8; DB 10; Length 896;									
Best Local Similarity 82.1%; Pred. No. 3.4e-159;									
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps									
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QY	486	GTTAGTGCAGAGATAGATATATGCAAGAGAGGGGAATGGAGTTGCAACAATAAAT	545						
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Db									
QY	546	GTACCTGGCAGCAAGATAGCCGAAGCGGCCAGATTGAATCCGACCACGAGGAATCCAG	605						
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; Sequence 3, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic

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; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000940US
; CURRENT APPLICATION NUMBER: US/09/981.087A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-981-087A-1

Query Match 15.5%; Score 148.4; DB 9; Length 1062;
Best Local Similarity 56.5%; Pred. No. 1.2e-36;
Matches 297; Conservative 0; Mismatches 226; Indels 3; Gaps 1;

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Qy	181	CTTCTGCAAAACGCGCAATGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGTG	240
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GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

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Title: US-09-978-382A-5

Perfect score: 959

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Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
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; Sequence 7, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Fannadiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 959 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 78..818
; NAME/KEY: misc.feature
; LOCATION: 1..959
; OTHER INFORMATION: /note= "AGL5 cDNA and deduced
; OTHER INFORMATION: protein sequences."
US-09-067-800-7

Query Match		100.0%;	Score 959;	DB 4;	Length 959;	
Best Local Similarity		100.0%;	Pred. No. 0;			
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QY	61	AGCTAGGGCTTATAGAAATGGAGGGTGGTGGAGTAATGAAGTAGCAGAGAGAGCAAGA	120			
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QY	481	ACTTTAAGGAACCTCAAGAACCTTCAAAAGTAGGCTTGAGAAAGGAAATCAGTGTGCCGAT	540			
DB	481	ACTTTAAGGAACCTCAAGAACCTTCAAAAGTAGGCTTGAGAAAGGAAATCAGTGTGCCGAT	540			
QY	541	CCAAGAAGCAGAGATGTTAGTTCGAGAGATTGAATACATGCAAAAAGGAAATCGAGC	600			
DB	541	CCAAGAAGCAGAGATGTTAGTTCGAGAGATTGAATACATGCAAAAAGGAAATCGAGC	600			
QY	601	TGCAAAACGATATCATCTCCGCTCCAGATTACTGAAAGAACAGGTCTACAGCAAC	660			
DB	601	TGCAAAACGATATCATCTCCGCTCCAGATTACTGAAAGAACAGGTCTACAGCAAC	660			
QY	661	AAGATCGAGTGTGATACATCAAGGAGAGTTTACGAGTCGGGTGTTACTTCTTCTCACC	720			
DB	661	AAGATCGAGTGTGATACATCAAGGAGAGTTTACGAGTCGGGTGTTACTTCTTCTCACC	720			
QY	721	AGTCGGGCGAGTATAACCGGAATTATATTCGGGTTAACTTCTTGAACCGGAATCAGAAT	780			
DB	721	AGTCGGGCGAGTATAACCGGAATTATATTCGGGTTAACTTCTTGAACCGGAATCAGAAT	780			
QY	781	CCTCCACCAACGACCAACCTCTGCAACTGTTTGTGATTCAGTCTAACATAAGCTTCT	840			
DB	781	CCTCCACCAACGACCAACCTCTGCAACTGTTTGTGATTCAGTCTAACATAAGCTTCT	840			
QY	841	TCCTCAGCCTCAGATCGATCTATAGTGTACCTAAATGCGGCGGTCCTCAACATCTA	900			
DB	841	TCCTCAGCCTCAGATCGATCTATAGTGTACCTAAATGCGGCGGTCCTCAACATCTA	900			
QY	901	GTCGCAAGCTGAGGGGACCACTAGTGTCTATACGAACCTCCAGAGACGGTTACACAAA	959			
DB	901	GTCGCAAGCTGAGGGGACCACTAGTGTCTATACGAACCTCCAGAGACGGTTACACAAA	959			

GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Ferrandiz, Cristina
TITLE OF INVENTION: Seed Plants Characterized by Delayed
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,677
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/067,800
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2948
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 959 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 78..818
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..959
OTHER INFORMATION: /note= "AGL5 cDNA and deduced protein sequences."
US-09-349-677-7

Query Match		100.0%;	Score 959;	DB 4;	Length 959;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 959;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	GAATTTCATCTTCCCATCCTCCTCCTCTCTTTCTTCTGATCATATAATTAATCTTGCTAAGCC	60			
DB	1	GAATTTCATCTTCCCATCCTCCTCCTCTCTTTCTTCTGATCATATAATTAATCTTGCTAAGCC	60			
QY	61	AGCTAGGGCTTATAGAAATGGAGGGTGGTGGAGTAATGAAGTAGCAGAGAGCAAGA	120			
DB	61	AGCTAGGGCTTATAGAAATGGAGGGTGGTGGAGTAATGAAGTAGCAGAGAGCAAGA	120			
QY	121	AGATAGGGAGGAGGAGATAGAGATAAAGAGGATAGAGACACTACGAATCGTCAAGTCA	180			
DB	121	AGATAGGGAGGAGGAGATAGAGATAAAGAGGATAGAGACACTACGAATCGTCAAGTCA	180			
QY	181	CTTTCTGCAAAACGACCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTCTTTGTGTG	240			
DB	181	CTTTCTGCAAAACGACCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTCTTTGTGTG	240			
QY	241	ACGCTGAGGTTGCTTGTCTATCTTCTCATCTTCTCCACTCGAGGCGGCTCTACGAGTACGCCAACA	300			
DB	241	ACGCTGAGGTTGCTTGTCTATCTTCTCATCTTCTCCACTCGAGGCGGCTCTACGAGTACGCCAACA	300			

Db 606 TGTACATAAGGACGACAGTTTACGAATCCGGTGTATCTTCTCATGACCAGTCGACGA 665
QY 731 GTATAACCGGAATTATATTTGGGTTAACTTCTTTGAACCGGAATCAGAATTCCTCAACCA 790
Db 666 TTATAATCGGAACATATATTCGGTGAACCTTCTTTGAACCGGAATCAGCAATTCCTCGGCCA 725
QY 791 AGACCAACCACTCTCGAACCTGTGTTGATTGAGTCTAACAATAAGCTTCTT 840
Db 726 AGACCAACCTCTCTTCAACTGTGTAACTCAAAACATGATAACTTGTGTT 775

RESULT 4

US-09-349-677-5
; Sequence 5, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 896 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..753
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 896
; OTHER INFORMATION: /note="There is a poly(A) tail at
; OTHER INFORMATION: the end of the cDNA sequence."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..896
; OTHER INFORMATION: /note="AGLI cDNA and deduced
; OTHER INFORMATION: protein sequences."
; US-09-349-677-5

Query Match 56.0%; Score 536.8; DB 4; Length 896;
Best Local Similarity 82.1%; Pred. No. 4.6e-175;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 77 AATGAGGGTGGTCGAGTAATGAAGTAGCAGAGCAGCAAGAAGATAGGGAGGGAA 136
Db 6 AATGGAGGAAGGTGGGAGTAGTCACGAGCGAGAGTAGCAAGAAACTAGGGAGGGAA 65
QY 137 GATAGAGATAAGAGAGATAGAACACTAGCAATCGTCAAGTCACTTTCTTCCAAACGACG 196
Db 66 AATAGAGATAAGAGAGATAGAGAACACAAACAAATCGTCAAGTTACTTTCTGCAACGACG 125
QY 197 CAATGCTTTACTCAAGAAAGCTTATGAGCTCTCTGCTCTTGTGACGCTGAGTGTCTCT 256
Db 126 CAATGCTCTTCTCAAGAAAGCTTATGAACCTCTCTGCTCTTGTGATGCGGAGTTGCCT 185
QY 257 TGTATCTTCTTCCACCTCGAGCGCTCTTACGAGTAGCCCAACAAACAGTGTGAGAGAAC 316
Db 186 CGTCATCTTCTCCACCTCGTGGCGCTCTTATGATAGTCGCCCAACAAACAGTGTGAGGGGTAC 245
QY 317 AATAGAAAGGTACAAGAAAGCTTGTCTCCGAGCGGTTAACTCTCCGACCATCACCGGACG 376
Db 246 AATTGAAAGGTACAAGAAAGCTTGTCTCCGATGCGCTCAACCTCTTCCGTCACCGGACG 305
QY 377 TAATACTCAGTACTATCAGCAAGAGCGTCTAAACTCCGGAGACAGATTCCGGGACATTCA 436
Db 306 TAATACTCAGTACTATCAGCAAGAGCGTCTTAAGCTTCGGAGGCGAGATTCCGAGATATCA 365
QY 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCTTGAACCTTTAAGGAACTCAA 496
Db 366 GAATTTCAATAGGCATATCTTGGGGAATCCTTGGTTCTTGAACCTTCAAGGAACTCAA 425
QY 497 GAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCGGATCCCAAGAGCAGAGAT 556
Db 426 AAACCTAGAAGGAGCGTCTTGAAGAAAGGAATCAGCGGTGTCGCTCCAAAAGAAATGAGCT 485
QY 557 GTTAGTTGCAGAGATTGAATACATGCAAAAAGGAAATCGAGCTGCAAAAACGATAAAT 616
Db 486 GTTAGTGGCAGAGATAGATATATGCAGAGAGGGAATGAGTTGCAACAACAATAAAT 545
QY 617 GTATCTCCGCTCCAAGATTACTGAA-----AGAACAGGTCTACAGCAACAAGATCCAG 670
Db 546 GTACCTCGAGCAAAAGATAGCCGAAGGCGCAGATTGAATCCGGACCCAGGAAATCAG 605
QY 671 TGTGATACATCAAGGGACAGTTTACGAGTCGGGTGTTACTTCTTCTCACCAGTCGGGCA 730
Db 606 TGTGATACAGGGGACAGATTGAGGATCGGTTGATCTTCTCATGACCAGTCGACGA 665
QY 731 GTATAACCGGAATTATATTTGGGTTAACTTCTTTGAACCGGAATCAGAATTCCTCCAACA 790
Db 666 TTATAATCGGAACATATATTCGGTGAACCTTCTTGAACCGAATCAGCAATTCCTCGGCCA 725
QY 791 AGACCAACCACTCTGCAACTTGTGTTGATTCAGTCTAACAATAAGCTTCTT 840
Db 726 AGACCAACCTCTCTTCAACTGTGTAACTCAAAACATGATAACTTGTGTT 775

RESULT 5

US-09-067-800-4
; Sequence 4, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,800
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2948
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6138 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..6138
OTHER INFORMATION: /label= AGL5_promoter
OTHER INFORMATION: /note= "Nucleotide sequence of the AGL5 promoter."
US-09-067-800-4

Query Match 34.3%; Score 329; DB 4; Length 6138;
Best Local Similarity 100.0%; Pred. No. 8.6e-103;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 631 AGATTACTGAAGAAGAGGTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG 690
|||||
Db 5733 AGATTACTGAAGAAGAGGTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG 5792
QY 691 TTTAGAGTCGGGTCTTACTTCTTCACAGTCGCGGGCAGTATAACCGGAATTATATTG 750
|||||
Db 5793 TTTAGAGTCGGGTCTTACTTCTTCACAGTCGCGGGCAGTATAACCGGAATTATATTG 5852
QY 751 CGGTTAACTTCTTGAACCGAATCAGAAATCTCTCAACCAAGACCAACCACTCTGCAAC 810
|||||
Db 5853 CGGTTAACTTCTTGAACCGAATCAGAAATCTCTCAACCAAGACCAACCACTCTGCAAC 5912
QY 811 TTGTTGATTGAGTCTACATTAAGCTTCTTCTCAGCTGAGATCGATCTATAGTGCA 870
|||||
Db 5913 TTGTTGATTGAGTCTAAACATAAGCTTCTTCTCAGCTGAGATCGATCTATAGTGCA 5972
QY 871 CCTAAATCGCGCGGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGCA 930
|||||
Db 5973 CCTAAATCGCGCGGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGCA 6032
QY 931 TACGAACCTCCAAGAGACGGTTACACAAA 959
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Db 6033 TACGAACCTCCAAGAGACGGTTACACAAA 6061

RESULT 6
US-09-349-677-4
Sequence 4, Application US/09349677
Patent No. 6288305
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Ferrandiz, Cristina
TITLE OF INVENTION: Seed Plants Characterized by Delayed
TITLE OF INVENTION: Seed Dispersal
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,677
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/067,800
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2948
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6138 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..6138
OTHER INFORMATION: /label= AGL5_promoter
OTHER INFORMATION: /note= "Nucleotide sequence of the AGL5 promoter."
US-09-349-677-4
Query Match 34.3%; Score 329; DB 4; Length 6138;
Best Local Similarity 100.0%; Pred. No. 8.6e-103;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 631 AGATTACTGAAGAAGAGGTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG 690
|||||
Db 5733 AGATTACTGAAGAAGAGGTCTACAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAG 5792
QY 691 TTTACAGTCGGGTGTGTTACTTCTTCACAGTCGCGGGCAGTATAACCGGAATTATATTG 750
|||||
Db 5793 TTTACAGTCGGGTGTGTTACTTCTTCACAGTCGCGGGCAGTATAACCGGAATTATATTG 5852
QY 751 CGGTTAACTTCTTGAACCGAATCAGAAATCTCTCAACCAAGACCAACCACTCTGCAAC 810
|||||
Db 5853 CGGTTAACTTCTTGAACCGAATCAGAAATCTCTCAACCAAGACCAACCACTCTGCAAC 5912
QY 811 TTGTTGATTGAGTCTAAACATAAGCTTCTTCTCAGCTGAGATCGATCTATAGTGCA 870
|||||
Db 5913 TTGTTGATTGAGTCTAAACATAAGCTTCTTCTCAGCTGAGATCGATCTATAGTGCA 5972
QY 871 CCTAAATCGCGCGGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGCA 930
|||||
Db 5973 CCTAAATCGCGCGGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGCA 6032
QY 931 TACGAACCTCCAAGAGACGGTTACACAAA 959
|||||
Db 6033 TACGAACCTCCAAGAGACGGTTACACAAA 6061

RESULT 7
US-08-460-512-6
Sequence 6, Application US/08460512
Patent No. 5744693
GENERAL INFORMATION:
APPLICANT: MEYEROWITZ, Elliot M.
APPLICANT: YANOFKY, Martin F.
APPLICANT: MA, Hong
TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400

QY	117	AAGAAGATAGGGAGAGGAAGATAGAGATAAAGAGAGATAGAGAAACACTACGAATCGTCAA	176
Db	152	AGAAACTGGGAAGAGAAAGATTGAGATCAACCGGATCGAAACGACACAAACGAATCGTCAA	211
QY	177	GTCACTTCTGCAAAACGACGCAATGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTG	236
Db	212	GTCACTTCTGCAAAAGAGACCAATGGTTTACTCAAAAAGCGCTATGAATTACTGTGCTC	271
QY	237	TGTGACGCTGAGGTTGCTCTTGTGTCATCTTCTCCACTCGAGGCGCTCTACGAGTACGCC	296
Db	272	TGTGATGCTGAGGTTGCTTGTGTTCTCAAGCAGAGGCGAGACTCTATGAGTATGCC	331
QY	297	AACAACAGTCTGAGAGGAAACAATAGAAAGGTACAAGAAAGCTTGTCTCCACGCCGTTAAC	356
Db	332	AACAACAGTGTGAAGACACAATGAGAGGTACACAAGAGCTTGTTCAGATTCCTCAACAC	391
QY	357	CCCTCCGACCATCACCGAAGCTAATACTCAGTACTATCAGCAAGAGCGGTCTAACTCCGG	416
Db	392	ACTGGTTCAAATTTCCGAGGCCAATGCTCAGTATTATCAGCAAGAGCCCTCAACACTGCG	451
QY	417	AGACAGATCCGGACATTCAGAAATTTGAACAGACACATTTCTGGTCAATCTCTTGCTTCC	476
Db	452	GCACAAATGGAAATCTGCAGAAATCAGACAGCAACATGTTGGTGAATCACTGGCTGCA	511
QY	477	TTGAACITTTAAGGAATCAAGAACCTTTGAAAGTAGGCTTGAGAAAGGAATACGTCGTGTC	536
Db	512	CTGAGCCTCAGAGATCTGAAGAATCTGGAACAAAAAATTTGAAAAGAGCGCATTAGCAAAATC	571
QY	537	CGATCCAAAGACGACGAGATGTTAGTTGACAGAGATTGAATACATCGAAAAAGGGAATTC	596
Db	572	AGATCCAAAAGAAATGAGCTGCTGTTTGTGTAATTTAGTGTACATGCAGAGAGGGAATTC	631

Db 340 TCGCAAAATTGGTAATTTCGAGAAATTCACAGGAAATATGTGGGTGAATCACTTAGTGCA 399
QY 477 TTGAACCTTTAAGGAACCTCAAGAACTTGAAGTAGGCTTGAGAAGGAATCAGTCGTGC 536
Db 400 TTGAGTGTGAAGAACTTAAGAGCTTGGAGATTAACCTTGAGAAGGAATTGGTGAAT 459
QY 537 CGATCCAGAAGCAGAGATGTGTTAGTTGTCAGAGATTGAATACATGCAAAAAGGGAATC 596
Db 460 CGTTCGAAAAGAAATGAGCTGTGTTGCTGAAATTCAGTATATGCAGAAGAGGAGATT 519
QY 597 GAGCTGCAAAACGATACATGTATCTCCGCTCCAGAGATTACTGAAA 642
Db 520 GACTTGCACAAATACACAGCTTCTCCGAGCAAGAAATGCAGAGA 565

RESULT 9
US-09-410-464-14
; Sequence 14, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1159
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (99)..(815)
US-09-410-464-14

Query Match 30.0%; Score 287.6; DB 4; Length 1159;
Best Local Similarity 71.7%; Pred. No. 5.6e-89;
Matches 377; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 117 AAGAAGTAGGGAGGGAAGATAGAGATAAAGAGATAGAGAACACTACGAATCGTCAA 176
Db 138 AGGAAGCTGGGGAGGGAAGGTGGAGATCAAGCGGATCGAGAACACCACCAATCGCAA 197
QY 177 GTCACCTTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTG 236
Db 198 GTCACCTTCTGCAAAAGCGGAATGGTTTGTCTCAAGAAAGCCTATGAATATCTGTTCTT 257
QY 237 TGTGACGCTGAGGTTGCTCTTGTCTATCTTCTCACTTCGAGGCGCTCTACGAGTAGCGC 296
Db 258 TGGATGCTGAGGTTGCACTCATCTCTCTCCAGCGGTGGAGCGCTTATGAGTACTCT 317
QY 297 AACACAGTGTGAGGGAACAAATAGAAAGGTACAGAAAGCTTGTCTCCGACGCGGTTAAC 356
Db 318 AACAAATAGTGTCAAATCTACAATTTGAAAGGTACAAAAGGCATGTGCAGATTCTTCCAAC 377
QY 357 CCTCCGACCATCCCGAGCTTAATACTCAGTACTATCAGCAAGAGCGGCTTAACTCCGG 416
Db 378 ACGGGTCAGTTTCTGAAGCAATGCTCAGTTCTATCAGCAAGAGCTGCCAAGCTGCGC 437
QY 417 AGACAGATTGGGACATTCAGAAATTTGAACAGACACATCTCTTGGTGAATCTTGGTTCC 476
Db 438 TCGCAAAATGGTAATTTCCAGAAATTCACAGGAATATGCTGGTGAATCACTTAGTGCA 497
QY 477 TTGAACCTTTAAGGAACCTCAAGAACTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGC 536
Db 498 TTGAGTGTGAAGGAACCTTAAGAGCTTGAAGATTAACCTTGAAGAAAGGAATTTGTAAT 557

QY 537 CGATCCAGAAGCAGAGATGTTAGTTGTCAGAGATTGAATACATGCAAAAAGGGAATC 596
Db 558 CGTTCGAAAAGAAATGAGCTGTGTTGCTGAAATTTGAGTATATGCAGAAGAGGAGATT 617
QY 597 GAGCTGCAAAACGATAACATGATCTCCGCTCCAGAGATTACTGAAA 642
Db 618 GACTTGCACAAATACACAGCTTCTCCGAGCAAGAAATGCAGAGA 663

RESULT 10
US-09-410-464-11
; Sequence 11, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER FILING DATE: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(723)
US-09-410-464-11

Query Match 29.7%; Score 284.4; DB 4; Length 723;
Best Local Similarity 71.3%; Pred. No. 5.3e-88;
Matches 375; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 117 AAGAAGTAGGGAGGGAAGATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAA 176
Db 40 AGGAAGCTGGGAAGGGGAAAGGTGGAGATCAAGCGGATCGAGAACACCACCAATCGCAA 99
QY 177 GTCACCTTCTGCAAAACGACCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTG 236
Db 100 GTCACCTTCTGCAAAAGCGCAGTGGTTGCTCAAGAAAGCCTACGAATATCTGTTCTT 159
QY 237 TGTGACGCTGAGGTTGCTCTTGTCTATCTTCTCACTTCGAGGCGCTCTACGAGTAGCGC 296
Db 160 TGGATGCTGAGGTTGCACTCATCTTCTTCTAGCCGCTGCGCTTATGAGTACTCT 219
QY 297 AACACAGTGTGAGAGGAACAATAGAAAGGTACAGAAAGCTTGTCTCCGACGCGCTTAAC 356
Db 220 AACGATAGTGTCAAATCAACAATTTGAGAGGTACAAAAGGCATCTGCAGATTCTTCAAAC 279
QY 357 CCTCCGACCATCACCGAAGCTAATACTCACTACTATCAGCAAGAGCGCTCTAACTCCGG 416
Db 280 ACTGGTCTGTTCTGAAGCAATGCTCAGTACTTACAGCAAGAGCTGCCAAGCTGGCT 339
QY 417 AGACAGATTGGGACATTCAGAAATTTGAACAGACACATCTTGTGTGAATCTCTTGGTTCC 476
Db 340 TCCCAAAATGGTAATTTGCAGAATTTCAAACAGGCATATGCTGGGTGAAGCGCTTAGTTCA 399
QY 477 TTGAACCTTTAAGGAACCTCAAGAACTTGAAGTAGGCTTGAAGAAAGGAATCAGTCGTGC 536
Db 400 TTGAGTGTGAAGGAACCTTAAGAGTTTGGAAATACGAGTTTGAAGAAAGGAATTAAGCAGA 459
QY 537 CGATCCAGAAGCAGAGATGTTAGTTGTCAGAGATTGAATACATGCAAAAAGGGAATC 596
Db 460 CGTTCGAAAAGAAATGAGCTGTGTTTGCAGAAATCAGTATATGCAGAAGAGGAGGTT 519
QY 597 GAGCTGCAAAACGATAACATGATCTCCGCTCCAGAGATTACTGAAA 642

Db 520 GACTTGCAACAATAACCAGCTTCTCCGAGCAAGATTCACAGAGA 565

RESULT 11
US-09-410-464-10
; Sequence 10, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1219
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(921)
US-09-410-464-10

Query Match 29.7%; Score 284.4; DB 4; Length 1219;
Best Local Similarity 71.3%; Pred. No. 7.4e-88;
Matches 375; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

Qy 117 AAGAAGATAGGGAGGGAACATAGAGATAAGAGGATAGAGAACACTACGAATCGTCAA 176
Db 235 AGGAAGCTGGGAAGGGAAAGGTGGAGATCAAGCGGATCGAGAACACCACCAATCGCCAA 294
Qy 177 GTCACCTTCTCAACACGACGCAATGGTTTACTCAAGAAGCTTATGAGCTCTCTGCTTTG 236
Db 295 GTCACCTTCTCAACACGACGCAATGGTTTACTCAAGAAGCTTATGAGCTCTCTGCTTTG 354
Qy 237 TGTGACGCTGAGGTGCTTGTGTCATCTTCCTCACTCAGAGCGGCTCTACAGTACGCC 296
Db 355 TGCATGCTGAGGTGCACTCATCTCTCTCTAGCCGGCTCGCTTTATGAGTACTCT 414
Qy 297 AACACAGCTGTCAGAGGACAAATAGAAAGGTACAAAGCTTGTCTCCGACCGCTTAAC 356
Db 415 AACGATAGTGCAAAATCAACAAATGAGAGGTACAAAAGGCAATCTGCAGATTTCTCAAC 474
Qy 357 CCTCCGACCATCACCAGAGCTAATACTCAGTACTATCAGCAAGAGCGGTCTAAACTCCGG 416
Db 475 ACTGGTCTGTTTCTGAAGCCAATGCTCAGTACTACCAGCAAGAGCTGCCAAGCTGCGT 534
Qy 417 AGACAGATTCGGGACATTCAGAAATTTGAACAGACACATTCCTTGGTCAATCTCTGGTTCC 476
Db 535 TCCCAAAATGTAATTTGCAGAAATTCAAACAGGCATATGCTGGGTGAAGCGCTAGTTCA 594
Qy 477 TTGAACCTTAAGGAACCTCAAGACCTTGAAAGTAGCTTGAGAAAGGAATCAGTCTGTTC 536
Db 595 TTGAGTGTGAGGAACCTTAAGATTTGGAATACGACTTGAGAAAGGAATACGACAAT 654
Qy 537 CGATCCAAAGAGCAGCAGATGTTAGTTGAGAGATTTGAATACATGCAGAAAGGGAATC 596
Db 655 CGTTCAAAAGAAATGAGCTGTTGTTTGCAGAAATCGAGTATATGCAGAGAGGAGGTT 714
Qy 597 GAGCTGCAAAACGATAACATGATGATCTCCGCTCCAGATTTACTGAA 642
Db 715 GACTTGCAACAATAAACCAAGCTTCTCCGAGCAAGATTTACAGAGA 760

RESULT 12
US-09-433-579-1
; Sequence 1, Application US/09433579

; Patent No. 6444877
; GENERAL INFORMATION:
; APPLICANT: Rottmann, William H.
; TITLE OF INVENTION: LSAG Gene
; FILE REFERENCE: LSAG Gene
; CURRENT APPLICATION NUMBER: US/09/433,579
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1297
; TYPE: DNA
; ORGANISM: Liquidambar styraciflua
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (331)..(1008)
US-09-433-579-1

Query Match 29.3%; Score 280.6; DB 4; Length 1297;
Best Local Similarity 69.8%; Pred. No. 1.6e-86;
Matches 379; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 120 AGATAGGAGAGGGAAGATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAAGTC 179
Db 328 AAAATGGGTAGGGGAAAGATCGAGATCAAGCGGATCGAGAACACGACCAACCGCAAGTC 387
Qy 180 ACUTTTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGT 239
Db 388 ACCTTCTGTAAGCGCGCAACGGCTTACTCAAGAGGCCATGAATATCTGTCTCTGT 447
Qy 240 GAGCTGAGGTGCTCTGTGTCATCTTCTCCACTCGAGGCGCTCTCTACGAGTACGCCAAC 299
Db 448 GATGCGGAGGTAGCCCTTATCGTCTTCTTACCCTGTCGCGCTTACGAGTATGCCAAC 507
Qy 300 AACAGTGTGAGAGGAACAATAGAAAGGTACAAAGAACTTGTCTCCGACCGCTTAAACCT 359
Db 508 AACAGTGTTAAGCAACAATGAGAGGTATAGAGGCACTGTGGATTCTCTCCAATACT 567
Qy 360 CGACCATCACCGAAGCTAATACTAGTACTATCAGCAAGAGCGCTTAAACTCGGAGA 419
Db 568 GGATCTGTTTCTGAAGCCAATGCTCAGTTCTACCAGCAAGAGCTGGCAAACTGCGTAAC 627
Qy 420 CAGATTCGGGACATTCAGAAATTTCAACAGACACATCTTGGTGAATCTCTTGGTTCCTTG 479
Db 628 CAAATCAGGAATATGCAGATACAAACAGGACTATGCTGGGTGAGTCTTTGGGCTCTCTG 687
Qy 480 AACTTTAAGGAACCTCAAGAACCTTTGAAAGTAGGCTTGAGAAAGGAATCAGTGTGTCCGA 539
Db 688 AGTCCCAAGAACTCAAGGGTCTGAGACTAAATTAGAGAAAGGCATTAGCAAAATAAGG 747
Qy 540 TCCAAGAGCAGCAGATGTTAGTTGCAGAGATTGAATACATGCRAAAAGGAAATCGAG 599
Db 748 TCCAAAAGAAATGAGCTACTGTTTTCGAAATGAATACATGCRAAAAGGAGGAAATCGAC 807
Qy 600 CTGCAAAACGATACATGATCTCCGCTCCAGATTTACTGAAAGAACAGGCTCTACAGCAA 659
Db 808 TTGCACAAATGATAACCAAGTATCTCCGACCAAAATAGCTGACACGAGAGAGCTCAACAG 867
Qy 660 CAA 662
Db 868 CAA 870

RESULT 13
US-08-460-512-3
; Sequence 3, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFKY, Martin F.
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,512
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/293,278
FILING DATE:
APPLICATION NUMBER: US/07/956,694
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57322/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1097 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 126..884
PS-08-460-512-3

Query Match	29.2%	Score 279.6;	DB 1;	Length 1097;
Best Local Similarity	70.7%;	Pred. No. 3.1e-86;		
Matches 372;	Conservative 0;	Mismatches 154;	Indels 0;	Gaps 0;
QY	117	AAGAAAGATAGGGAGAGGAAGATAGAGATAAAGAGGATAGAGAACTACGAATCGTCAA	176	
Db	168	AGAAAGCTGGGAGAGAAAGATCGAATTAACGGATCGAAACACACACGACCGTCAA	227	
QY	177	GTCACTTCTGCAACGACCGAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTG	236	
Db	228	GTTACTTCTTGCAACCGACGAAATGGTTGCTCAAGAAAGCTTACGAACCTCTCTGTCTTT	287	
QY	237	TGTGAGCGCTGAGGTGCTCTTGTCATCTTCTCCACTCGAGCGCTCTCTAGGATAGGCC	296	
Db	288	TGTGATGTGAAGTCGCACCTATTGCTCTCTAGCCGTGGCCGCTCTATGAGATACTCA	347	
QY	297	AACAACAGTGTGAGAGAACAAATAGAAAGGTACAAGAAAGCTTGCTCCGACGCCGTTAAAC	356	
Db	348	AACAACAGTGTAAAGGGAGCAATTGAGAGGTACAAGAAAGCAATATCCGATAATCTAAC	407	
QY	357	CCPCCGACCATTACCGAAGCTAATACCTCAGTACTATCAGCAAGAGCGCTCTAACTCCGG	416	
Db	408	ACCGATCCGTGCAGNAATTATGCACAGTATTATCAAGAATCTGCCAATTCGGT	467	
QY	417	AGACAGATTGGGACATTCAGAATTTGAACAGACACAACTCTTGSTGAATCTCTTGTTCC	476	
Db	468	CAACAAATTTATCAGCATACAGAACTCGAACAGGCAATTGATGGGTGAGAGATTGGGTCA	527	
QY	477	TTCAACTTTTAAAGGAACCTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGC	536	
Db	528	ATGCTCCCCAAGAGCTCAGGAACCTTGGAAAGCGAGATTAGACAGAAGTGTTAATCGAATC	587	
QY	537	CGATCCAAGAACGACGAGATGTTAGTTGTCAGAGATTCAATACATGCAAAAAGGGAATC	596	

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Db      588 CGATCCAAAGAAGCAACTTTATTTCGCCGAATTGACTACATCGACAAGAGAAGTT 647
        ||||| ||||| |||| | ||| | ||| ||||| ||||| ||||| |||||
QY      597 GAGCTGCAAAACGATACATGTATCTCCGTCCTCCAAGATTACTGAAA 642
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Db      648 GATTTCATAACGATAACCAGCTTCTTCGTGCTAAGATAGCTGAAA 693
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RESULT 14
US-08-460-512-1
; Sequence 1, Application US/08460512
; Patent No. 5744693
; GENERAL INFORMATION:
; APPLICANT: MEYEROWITZ, Elliot M.
; APPLICANT: YANOFSKY, Martin F.
; APPLICANT: MA, Hong
; TITLE OF INVENTION: PLANTS HAVING ALTERED FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,512
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,278
; FILING DATE:
; APPLICATION NUMBER: US/07/956,694
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57322/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 416..1270
; US-08-460-512-1

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	Query Match	28.5%;	Score 273.2;	DB 1;	Length 1457;
	Best Local Similarity	70.0%;	Pred. No. 6.le-84;		
	Matches 368;	Conservative	0;	Mismatches 158;	Indels 0;
QY	117	AGGAAGATAGGAGGAGCGAAGATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAA	176		
Db	557	AGGAATCTGGGAGAGGAAGATCGAATCAACGGGATCGAGAACACACGAATCGTCAA	616		
QY	177	GTCACTTTCTGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTTG	236		
Db	617	GTCACTTTTTCGAACGCTAGAGAAATGGTTTGTCTCAAGAAAGCTTACGAGCTCTCTGTCTC	676		
QY	237	TGTGACCGCTGAGTTGCTTTGTGTCATCTTCCTACTCGAGGCCGTCTCTACGAGTACGCC	296		
Db	677	TGTGATCGTGAAGTCGACACTCATGGTTTCTCTACGCGTGGTCGTCTCATGAGTACFCT	736		

QY 297 AACACAGCTGTGAGAGCAACATAGAAAGGTACAAAGCTTGTCCGACGCCGTTTAAAC 356
Db 737 AACACAGCTGTAAAAGGTACTATTGAGAGGTACAAGAGGCAATATCGGCAATTTCTTAAAC 796
QY 357 CCTCCGACCATCACCGAAGCTTAATCTCAGTACTATCAGCAAGAGCGCTTAAACTCCGG 416
Db 797 ACCGGATCGGTGGCAGAAATTAATGCACAGTATTATCAACAAGAAATCAGCCAAATTCGCT 856
QY 417 AGACAGATTCGGGACATTCAGAAATTTGAACAGACACATCTTTGGTGAATCTCTTGGTTCC 476
Db 857 CAACAAATTTATCAGCATACAAAACTCCACAGGCAATTTGATGGGTGAGACGATAGGGTCA 916
QY 477 TTGAACCTTTAAGGAACCTCAAGAACTTCAAAAGTGGCTTGAGAAAGGAATCAGTCGTGC 536
Db 917 ATGCTCCCAAGAGCTCAGGAACCTTGAAGAGCGCATAGAGAGAAATATTACCGAATC 976
QY 537 CGATCCAGAAAGCAGAGATTTAGTTTCAGAGATTTGAATACATCAAAAAAGGAAATC 596
Db 977 CGATCCAGAAAGATGAGCTCTTATTTTCTGAAATCGACTACATGCAGAAAAGAGAAGTT 1036
QY 597 GAGCTGCAAAAGCATACATGATCTCCGCTCCAGATTAAGTAA 642
Db 1037 GATTGCAATACGATAACAGATTCTTCGTGCAAGATAGCTGAAA 1082

RESULT 15

US-09-067-800-3
; Sequence 3, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..5622
; OTHER INFORMATION: /label= AGLI-promoter
; OTHER INFORMATION: /note= "Nucleotide sequence of the AGLI promoter."
US-09-067-800-3

Query Match

19.6%; Score 188; DB 4; Length 5622;

Best Local Similarity 89.0%; Pred. No. 3.8e-54;
Matches 203; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 77 AATGGAGGTGGTGGGAGTAATGAAGTAGCAGAGAGCAGCAAGAGATAGGGAGAGGAA 136
Db 2605 AATGGAGGAAGTGGGAGTAGTCACGACGAGAGAGTAGCAAGAAACTAGGGAGAGGAA 2664
QY 137 GATAGAGATAAAGAGGATAGAGAACACTACGAAATCGTCAAGTCACTTTCTGCAAAACGACG 196
Db 2665 AATAGAGATAAAGAGGATAGAGAACACACAAATCGTCAAGTTACTTTCTGCAAAACGACG 2724
QY 197 CAATGGTTTACTCAAGAAAGCTTTATGAGCTCTCTGTCTTTGTGTGACGCTGAGGTGCTCT 256
Db 2725 CAATGGTCTTTCTCAAGAAAGCTTTATGAACCTCTCTGTCTTTGTGTGATGCGGAAGTTGCCCT 2784
QY 257 TGTCTCTCTCTCCACTCGAGCGCGTCTCTAGGATAGGCCCAACACAG 304
Db 2785 CGTCATCTCTCTCCACTCGTGGCGGTCTCTATGAGTAGCCCAACACAG 2832
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 05:45:28 ; Search time 237.294 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23:	/SID22/gcgdata/geneseq/geneqseq-emb1/NA2001B.DAT:*			
24:	/SID22/gcgdata/geneseq/geneqseq-emb1/NA2002.DAT:*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	959	100.0	959	20 AAV99860	Arabidopsis AGL5 C
2	735	76.6	777	21 AAC43464	Arabidopsis thalia
3	538	56.1	1202	21 AAC34634	Arabidopsis thalia
4	536.8	56.0	896	20 AAV99859	Arabidopsis AGL1 C
5	475.4	49.6	511	21 AAC33755	Arabidopsis thalia
6	465	48.5	511	21 AAC45357	Arabidopsis thalia
7	329	34.3	6138	20 AAV99858	Arabidopsis AGL5 g
8	329	34.3	6138	24 AAV77275	Arabidopsis dehisc
9	305.8	31.9	1143	17 AAT34428	Eucalyptus AGE1 cD

10	287.6	30.0	714	22 AAF85402	Nucleotide sequenc
11	287.6	30.0	1115	21 AAZ57949	Poplar floral home
12	287.6	30.0	1159	22 AAF85401	Nucleotide sequenc
13	287.6	30.0	1159	24 ABK88491	Poplar floral home
14	285.4	29.8	1157	21 AAZ50201	Petunia hybrida ne
15	285.4	29.8	1157	21 AAZ35494	Petunia nectary-sp
16	284.4	29.7	723	22 AAF85399	Nucleotide sequenc
17	284.4	29.7	1201	21 AAZ57947	Poplar floral home
18	284.4	29.7	1219	22 AAF85398	Nucleotide sequenc
19	284.4	29.7	1219	24 ABK88489	Poplar floral home
20	273.2	28.5	903	21 AAC51039	Arabidopsis thalia
21	270	28.2	1053	21 AAC46362	Arabidopsis thalia
22	270	28.2	1057	21 AAC37453	Arabidopsis thalia
23	268.8	28.0	997	17 AAT34432	Eucalyptus AGE2 cD
24	264.8	27.6	706	21 AAC55965	Eucalyptus grandis
25	255.6	26.7	909	21 AAA9364	Plant PrAG1 promot
26	252.6	26.3	1218	21 AAC43678	Zea mays DNA fragm
27	252	26.3	805	24 ABK82084	DNA encoding novel
28	252	26.3	1259	24 ABK82131	DNA encoding novel
29	242.6	25.3	1321	21 AAC47718	Zea mays DNA fragm
30	219	22.8	581	21 AAC57270	Eucalyptus grandis
31	188	19.6	466	21 AAC35890	Zea mays DNA fragm
32	188	19.6	5622	20 AAV99857	Arabidopsis AGL1 q
33	188	19.6	5622	24 AAT77274	Arabidopsis dehisc
34	186.2	19.4	845	24 ABK98876	Arabidopsis thalia
35	161.6	16.9	457	21 AAC41474	Zea mays DNA fragm
36	159.2	16.6	352	21 AAC55878	Eucalyptus grandis
37	159	16.6	1144	19 AAV18014	Pinus radiata cone
38	156.4	16.3	423	21 AAC56741	Eucalyptus grandis
39	152.6	15.9	1075	21 AAC46463	Arabidopsis thalia
40	150.4	15.7	498	20 AAV69758	Tobacco ovary-spec
41	148.4	15.5	1062	20 AAV18594	Arabidopsis AGL8 n
42	148.4	15.5	1062	20 AAV99856	Arabidopsis AGL8-1
43	147.6	15.4	1044	20 AAV71739	Rice OsMADS6 cDNA.
44	147.6	15.4	1044	21 AAL44853	Plant flowering ti
45	146.8	15.3	1123	21 AAC41877	Arabidopsis thalia

ALIGNMENTS

RESULT 1
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ID AAV99860 standard; cDNA; 959 BP.
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AC AAV99860;
XX
DT 10-MAY-1999 (first entry)
XX
DE Arabidopsis AGL5 cDNA.
XX
KW AGL5-like gene; agamous-like 5 gene; seed dispersal; dehiscence;
KW transgenic plant; promoter; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key
FT CDS
FT 78..818
FT /*tag= a
XX
PN WO9900502-A1.
XX
PD 07-JAN-1999.
XX
PF 25-JUN-1998; 98WO-US13208.
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PR 28-APR-1998; 98US-0067800.
PR 27-JUN-1997; 97US-0051030.
XX
PA (RECC) UNIV CALIFORNIA.
XX
PI Ferrandiz C, Yanofsky MF;
XX

PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
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PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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Query Match 56.18; Score 538; DB 21; Length 1202;

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Db 621 TAATACCTCAGTACTATCAGCAAGAGCGCTCTAAGCTTCGGAGGAGATTCGAGATATTC 680
QY 437 GAATTTGAACAGACACATCTTGGTGAATCTCTGGTTCCTTGAACCTTAAGGAAGTCA 496
Db 681 GAATTTGAACAGACACATCTTGGTGAATCTCTGGTTCCTTGAACCTTAAGGAAGTCA 740
QY 497 GAACCTTGAAGTAGGCTTGAGAAGGAATCAGTCGTCTCCGATCCCAAGAACGAGAT 556
Db 741 AAACCTAGAGGAGCTCTTGAAAGGAATCAGCGGTCTCCGCTCCCAAGGAATGAGCT 800
QY 557 GTTAGTTGCAGAGATTGAATACATGCAAAAGGAATCAGCTGCAAAAGGATCAAT 616
Db 801 GTTAGTTGCAGAGATTGAATACATGCAAAAGGAATCAGCTGCAAAAGGATCAAT 860
QY 617 GTATCTCCGCTCCAGATTAAGTAA-----AGAACAGGTCTACAGCAACCAAGAAATCGAG 670
Db 861 GTACCTCGAGCAAGATAGCCGAAGGCGCCAGATGTAATCCGGACACAGGAATCGAG 920
QY 671 TGTGATACATCAAGGAGCAGTTTACGAGTCGGGTGTTTACTTCTTCTCACCAGTCGGGCA 730
Db 921 TGTGATACATCAAGGAGCAGTTTACGAGTCGGGTGTTTACTTCTTCTCACCAGTCGGGCA 980
QY 731 GTATAACCGGAATTAATTCGGGTTAACCTTCTTGAACCGGAATCAGATTCCTCCAACCA 790
Db 981 TTATAATCGGAATTAATTCGGGTTAACCTTCTTGAACCGGAATCAGATTCCTCCAACCA 1040
QY 791 AGACCAACCACTCTGCAACTTGTGTTGATTCAGTCTAACATCAAGCTTCTT 840
Db 1041 AGACCAACCACTCTTCAACTTGTGTTGATTCAGTCTAACATCAAGCTTCTT 1090

RESULT 4
AAV99859
ID AAV99859 standard; cdNA; 896 BP.
AC AAV99859;
XX
AC AAV99859;
XX
DT 10-MAY-1999 (first entry)
XX
DE Arabidopsis AGL1 cdNA.
XX
KW AGL1-like gene; agamous-like 1 gene; seed dispersal; dehiscence;
KW transgenic plant; promoter; ss.
XX
OS Arabidopsis thaliana.

Key	Location/Qualifiers
CD5	7..753
polyA_site	/*tag= a 896
	/*tag= b
WO9900502-A1.	
PN	
XX	
PD	07-JAN-1999.
XX	
PF	25-JUN-1998; 98WO-US13208.
XX	
PR	28-APR-1998; 98US-0067800.
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PR	27-JUN-1997; 97US-0051030.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Ferrandiz C, Yanofsky MF;
XX	
DR	WPI; 1999-095747/08.
XX	
DR	P-PSDB; AAW80999.
XX	

PT Use of agamous-like nucleic acids - useful for the production of
PT transgenic seed plants in which dehiscence is modified resulting in
XX delayed seed dispersal
XX Disclosure: Page 87-88; 126pp; English.
CC This is the nucleotide sequence of an Arabidopsis agamous-like 1
CC (AGL1) gene cDNA clone that codes for AGL1 polypeptide (see
CC AAW80999) which is involved in the regulation of dehiscence. The
CC invention provides a transgenic seed plant, such as an agli and
CC agl5 double mutant, that is characterised by delayed seed dispersal
CC due to suppression of AGL1 and AGL5 (see AAV99860) expression. The
CC invention also provides dehiscence zone regulatory elements, derived
CC from the AGL1 or AGL5 gene (see AAV99857 and AAV99858), that confer
CC selective expression upon an operatively linked nucleic acid
CC molecule in the valve margin or dehiscence zone of a seed plant.
CC The transgenic seed plants include members of the Brassicaceae,
CC such as rapeseed, and members of the Fabaceae, such as soybean,
CC pea, lentil and bean. A plant expression vector comprising a
CC dehiscence zone-selective regulatory element, and a kit for
CC producing the transgenic seed plants are also provided.
XX
SQ Sequence 896 BP; 285 A; 186 C; 205 G; 220 T; 0 other;

Query Match 56.0%; Score 536.8; DB 20; Length 896;
Best Local Similarity 82.1%; Pred. No. 5.7e-156;
Matches 632; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 77 AATGGAGGGTGGTCCGAGTAATGAAGTACGAGAGCAGCAAGAGATAGGAGAGGAA 136
Db 6 AATGGAGGAAGTGGGAGTAGTCACGACGAGAGAGTAGCAAGAACTAGGAGAGGAA 65
QY 137 GATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAAGTCACTTTCTGCAACGACG 196
Db 66 AATAGAGATAAAGAGGATAGAGAACCAACAATACTGCTACTTTCTGCAACGACG 125
QY 197 CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTGTGTGACGCTGAGGTGCTCT 256
Db 126 CAATGGTCTTCTCAAGAAAGCTTATGAACCTCTCTGTGTGTGATGCCGANGTTGCCCT 185
QY 257 TGTCACTTCTCCACTCGAGGCGGTCTCTACGAGTAGCCCAACAACAGTGTGAGAGGAAC 316
Db 186 CGTCATCTTCTCCACTCGTGGCGTCTCTATGAGTAGCCCAACAACAGTGTGAGGGGTAC 245
QY 317 AATAGAAAGGTACAAGAAAGCTTGTCTCCGAGCGCGTTAAACCTCCGACCATCAGGAAGC 376
Db 246 AATAGAAAGGTACAAGAAAGCTTGTCCGATGCGCTCAACCTCTTCCGTCACCGAAGC 305
QY 377 TAATACTCAGTACTATCAGCAAGAGGCGTCTAAACTCCGGAGACAGATTCGGGACATTC 436
Db 306 TAATACTCAGTACTATCAGCAAGAGGCGTCTAAAGCTTCGGAGGAGATTCGAGATATTC 365
QY 437 GAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCCTTGAACCTTAAAGGAACCTCAA 496
Db 366 GAATTTGAATAGGCATATTTGGGGAATCACTTGTTCCTTGAACCTTCAAGGAACCTCAA 425
QY 497 GAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTCGATCCCAAGACGACGAGAT 556
Db 426 AAACCTAGAAAGGAGCTCTTGAAGAAAGGAATCAGCGCTGTCCGCTCCCAAGAAAGTGAAGCT 485
QY 557 GTTAGTTGCAGAGATTGAATACATGCAAAAAGGAATTCGAGTGCAGGATCAAGGATTAACAT 616
Db 486 GTTAGTTGCAGAGATTGAATACATGCAAGAGGGAATTCGAGTGCAGGATTAACATTAACAT 545
QY 617 GTATCTCCGCTCCAGATTAATCTGAA-----AGAACAGGTCTACAGCAACCAAGAAATCGAG 670
Db 546 GTACCTCGAGCAAGATAGCCGAAGGCGCCAGATTTGAATCCGGACACAGCAAGAAATCGAG 605
QY 671 TGTGATACATCAAGGAGCAGTTTACGAGTCGGGTGTTTACTTCTTCTCACCAGTCGGGCA 730
Db 606 TGTGATACATCAAGGAGCAGGATTTACGAATCCGGGTGTTTACTTCTTCTCACCAGTCGGGCA 665
QY 731 GTATAACCGGAATTAATTCGGGTTAACTTCTTGAACCGGAATCAGAAATTCCTCCAACCA 790

QY	62	GCTAGGGCTTATAGAAATGGAGGGTGGTGGAGTAGTAAGTACGAGAGAGACCAAGAA	121
Db	95	GCTAGGGCTTATAGAAATGGAGGGTGGTGGAGTAGTAAGTACGAGAGAGACCAAGAA	154
QY	122	GATAGGGAGAGGGAAGATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAAGTCAC	181
Db	155	GATAGGGAGAGGGAAGATAGAGATAAAGAGGATAGAGAACACTACGAATCGTCAAGTCAC	214
QY	182	TTTCTGCAAAACGACGAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTGTGTGA	241
Db	215	TTTCTGCAAAACGACGAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTGTGTGA	274
QY	242	CGCTGAGTTGCTCTTGTGTCATCTTCTCCACTCGAGGCCGCTCTTACGAGTACGCCACAA	301
Db	275	CGCTGAGTTGCTCTTGTGTCATCTTCTCCACTCGAGGCCGCTCTTACGAGTACGCCACAA	334
QY	302	CAGTGTGAGAGGAACAATAGAAAGGTACAAAGAAAGCTTGTCTCCGACGCCGTTAACCCCTCC	361
Db	335	CAGTGTGAGAGGAACAATAGAAAGGTACAAAGAAAGCTTGTCTCCGACGCCGTTAACCCCTCC	394
QY	362	GACCATCACCGAAGCTAATACTCAGTACTATCAGCAAGAGCGTCTAAACTCCGGAGACA	421
Db	395	GACTATCACCGAAGCTAATACTCAGTACTATCAGCAAGAGCGTCTAAACTCCGGAGACA	454
QY	422	GATTCGGGACATTCAGAAATTTGACAGACACATCTTGGTGAATCTCTTGGTTCCCTT	478
Db	455	GATTCGGGACATTCAGAAATTTGACAGACACATCTTGGTGAATCTCTTGGTTCCCTT	511
RESULT 6			
AAC45357			
ID	AAC45357 standard; DNA; 511 BP.		
XX	AAC45357;		
XX	18-OCT-2000 (first entry)		
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 46222.		
KW	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway;		
XX	metabolic pathway; promoter; termination sequence; ss.		
OS	Arabidopsis thaliana.		
PN	EP1033405-A2.		
PD	06-SEP-2000.		
XX	25-FEB-2000; 2000EP-0301439.		
XX	25-FEB-1999; 99US-0121825.		
PR	05-MAR-1999; 99US-0123180.		
PR	09-MAR-1999; 99US-0123548.		
PR	23-MAR-1999; 99US-0125788.		
PR	25-MAR-1999; 99US-0126284.		
PR	29-MAR-1999; 99US-0126785.		
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PR	06-APR-1999; 99US-0128234.		
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PR 22-OCT-1999; 99US-0160980.


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XX AU9539013-A.
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XX 30-MAY-1996.
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XX 22-NOV-1994; 94AU-0009589.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Dennis ES, Harcourt RL, Kyozyuka J, Llewellyn D;
XX Peacock WJ, Southerton S;
XX
XX WPI: 1996-278411/29.
XX P-PSDB; AAR99633.
XX
XX Eucalyptus reproductive genes - useful for prodm. of sterile
XX Eucalyptus trees useful for establishing wood lot plantations or in
XX re-forestation projects
XX
XX Claim 8; Page 29-30; 60pp; English.
XX
XX A cdna clone (AAT34428), designated AGE1, is analogous to the
XX Arabidopsis agamous (AG) and Antirrhinum plena (PLE) flower
XX development genes. It was obtd. by PCR amplification of E.
XX globulus cdna using primers based on homologous regions of the
XX Arabidopsis and Antirrhinum genes, followed by a screening of a E.
XX globulus library. It codes for a protein, AGE-1 (AAR99633), that
XX shows homology to the AG and PLE proteins. AGE1 is very
XX highly expressed in mature flower buds. Another cdna clone,
XX AGE2 (AAT34432), was also identified. Antisense or ribozyme
XX constructs of AGE, or of FLE2 and SQE genes (see also AAT34426 and
XX AAT34429-31), can be used to produce sterile transgenic Eucalyptus
XX trees by minimising inflorescence.
XX
XX Sequence 1143 BP; 336 A; 244 C; 267 G; 296 T; 0 other;

Query Match 31.9%; Score 305.8; DB 17; Length 1143;
Best Local Similarity 71.8%; Pred. No. 3.1e-84;
Matches 400; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 126 GGGAGAGGGAACATAGAGTAAGAGGATAGAGACACTACGAATCGTCAAGTCACCTTC 185
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 186 TGCAACGACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTGTGTGACGCT 245
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 246 GAGGTTGCTCTTTCATCTTCTCCACTCGAGCGGCTCTCTAGAGTACGCCAACACAGT 305
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 366 ATCACCAGAGCTTAATACCTCAGTACTACTACGAAGAGCGGCTCTAAATCCGGAGACAGATT 425
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 565 RAGGATCTCAAGAACTCGAGAGCAAAATTAGAGAAATCGATCAGCCGAGTATAGATCAAG 624
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 546 AAGCAGCAGATGTTAGTTCGAGAGATTGAATACATGCAAAAAAGGAAATCGAGCTGCAA 605
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QY 625 AGAATGAGATGCTTTTGCCGAGATTGAGTACATGAGAGAGGAAATTGAGCTGCAA 684
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 606 AAGCATAACATGATCTCCGCTCCAGATTACTGAAGACACAGGTCTACAGCACACAGAA 665
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 685 AATGATAACATGATCTGAGAGCAAGATAGCTGAGAACGAGAGACACACAGCAGCAG 744
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 666 TCGAGTGTGATACATCA 682
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QY 745 CAGCAAGGGAGTGATCA 761
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
AAF85402
ID AAF85402 standard; cdna; 714 BP.
XX
XX AAF85402;
XX AC
XX
XX 23-JUL-2001 (first entry)
XX
XX Nucleotide sequence of the floral homeotic protein PTAG-2.
XX
XX Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;
XX LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
XX fertility; sterility; ss.
XX
XX Populus balsamifera.
XX
XX Key Location/Qualifiers
XX CDS 1..714
XX /*tag= a
XX /*product= "PTAG-2"
XX
XX CA2319853-A1.
XX
XX 01-APR-2001.
XX
XX 02-OCT-2000; 2000CA-2319853.
XX
XX 01-OCT-1999; 99US-0410464.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
XX
XX WPI: 2001-336098/36.
XX
XX P-PSDB; AAB68439.
XX
XX Novel isolated polynucleotide derived from Populus species, useful for
XX producing transgenic plants having modified fertility characteristic,
XX particularly sterility -
XX
XX Claim 25; Page 61-62; 69pp; English.
XX
XX The present sequence encodes a floral homeotic protein, designated
XX PTAG-2, which is derived from Populus balsamifera subsp. trichocarpa.
XX The specification also describes PTD, PTLF, and PTAG-1 proteins. The
XX floral homeotic proteins are expressed in floral tissues. PTLF is a
XX homologue of LEAFY (LFY) and FLORICAULA (FLO), and is expressed in
XX immature inflorescences on which floral primordia are developing. PTD
XX is a homologue of DEFICIENS (DEF), and is strongly expressed in stamen
XX primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
XX homologues of AGAMOUS (AG). The floral homeotic proteins and
XX polynucleotides are useful for producing transgenic plants having
XX modified fertility characteristics, particularly sterility.
XX
XX Sequence 714 BP; 223 A; 146 C; 172 G; 173 T; 0 other;

Query Match 30.0%; Score 287.6; DB 22; Length 714;
Best Local Similarity 71.7%; Pred. No. 1.1e-78;
Matches 377; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
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QY 477 TTGAACCTTTAAGGAACCTCAGAACCTTGAAGAGTAGGCTTGAGAAAGGAATCAGTCGTGTC 536
DB 533 CTGACTGCAGAAAGATCTGAAAGGCTGGAGACCAACCTTGAGAAAGGAATTTAGTAGAAT 592
QY 537 CGATCCAAAGACGAGAGTCTTGAAGTTCAGAGATTTGAATACATGCAAAAAGGGAATC 596
DB 593 AGGTCCAAAAGAAATGAATCCTCTTCTGCTGAGATTTGAGTATATGCGRAAAGGGAAT 652
QY 597 GAGTGCAGAAACGATAACATGTATCTCCGCTCCAGATTAATGAAAG 643
DB 653 GATTGACACAAACATCAGATCTCTGGGCAAGATAGCTGAGAG 699

RESULT 15
AAZ35494
ID AAZ35494 standard; cdNA; 1157 BP.

AC AAZ35494;

DT 11-APR-2000 (first entry)

DE Petunia nectary-specific FBPI5 cdNA.

KW FBPI4; nectary; nectar; transgenic plant; honey; ds.

XX Petunia hybrida.

OS Key Location/Qualifiers
FH 179..841
FT CDS /*Lag= a
FT

PN EP974667-A1.

XX 26-JAN-2000.

XX 16-JUL-1998; 98EP-0202375.

XX 16-JUL-1998; 98EP-0202375.

PR (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.

PA Creemers J, Angenent GC, Kater MM;

XX WPI; 2000-108400/10.

DR P-PSDB; AAY58648.

XX Novel DNA sequences used to produce modified honey, the metabolites of

PT which can be isolated and purified -

XX Claim 5; Page 17; 56pp; English.

XX The present sequence is that of Petunia hybrida strain W115 FBPI5
CC cDNA that was identified in nectary gland cDNA by differential
CC expression. The cDNA encodes a 221-amino acid MADS box protein
CC (see AAY58648) that is specifically expressed in the nectaries of
CC petunia. The present invention provides a method for producing
CC recombinant proteins in honey. The honey is manufactured by insects,
CC preferably honeybees, that collect the nectar of transgenic plants.
CC The FBPI5 gene and its promoter can be utilised in expression
CC cassettes for the production of transgenic plants that produce a
CC protein of interest in their nectar.

XX Sequence 1157 BP; 391 A; 203 C; 229 G; 334 T; 0 other;

Query Match 29.8%; Score 285.4; DB 21; Length 1157;
Best Local Similarity 71.3%; Pred. No. 6.8e-78;
Matches 376; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 117 AAGAGATAGGAGAGGGAAGATAGATTAAGAGGATAGAGACACTACGATCGTCAA 176
DB 173 AGGAAGATGGGAAGGAAGAAAGATTGAGATTGAAGATTAACAACAAATCGTCAA 232

QY 177 GTCACTTTCTGCAACGACGCAATGCTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTG 236
DB 233 GTCACTTTCTGTAAGAGAGAAATGGTTGCTTAAAAAGCTTATGAACCTTCTGTCTT 292
QY 237 TGTGACGCTGAGGTGCTCTTGTCTCTCCACTCGAGGCGCTCTCTACGAGTAGCGCC 296
DB 293 TGTGATGCTGAAAGTTGCTCTCATCGTTTTCTCAAGCGCTGGCGCCTCTATGAATATGCT 352
QY 297 ACAACAGTCTGAGAGGAACAATAGAAAGGTACAAGAAAGCTTGTCCGACGCGTTAAC 356
DB 353 AACACAGTGTGAAGGCAACAATTGATAGATATAAGAAAGCATCCCTCAGATTCTCCAAC 412
QY 357 CCTCGACCATCACCGAAGCTAATACTACTATCAGCAAGAGCGCTCTAAACTCCGG 416
DB 413 ACTGGATCTACTTCTGAAGCTAACACTCAGTTTTATCAACAAGAGCTGCCAAACTCCGA 472
QY 417 AGACAGATTCCGGACATTTGAGAAATTTGACAGACACATTTCTTGGTGAATCTCTGGTTCC 476
DB 473 GTTCAGATTGGTAACCTTACAGAACTCAACACAGGAACATGCTAGGCGAGTCTCTAAGTTCT 532
QY 477 TTGAACCTTTAAGGAACCTCAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCGTGTC 536
DB 533 CTCAGTGCAGAAAGATCTGAAGCGCTGGAGACCAACCTTGAGAAAGGAATTAGTAGAAT 592
QY 537 CGATCCAAAGACGAGAGATGTTAGTTGCAGAGATTGAATACATGCAAAAAGGGAATC 596
DB 593 AGGTCCAAAAGAAATGAACCTCTCTGCTGAGATTGAGTATATGCGAAAAAGGGAAT 652
QY 597 GAGTGCAGAAACGATAACATGTATCTCCGCTCCAGATTAATGAAAG 643
DB 653 GATTGACACAAACAATCAGATGCTTCGGGCAAGATAGCTGAGAG 699

Search completed: February 2, 2003, 08:19:19
Job time : 259.294 secs

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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 08:19:29 ; Search time 2626.26 Seconds
(without alignments)
10627.107 Million cell updates/sec

Title: US-09-978-382A-5
Perfect score: 959
Sequence: 1 gaattcatcttccatctctc.....ccaagagacggttacacaaa 959

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pi.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_man.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	959	100.0	959	6	ARI138348
2	959	100.0	963	8	ARI138348 Sequence
3	538	56.1	1202	8	ATHAGL5A
4	536.8	56.0	895	8	AY086196 Arabidopsis
5	536.8	56.0	896	6	ATHAGL1A
6	503.2	52.5	789	8	ARI138347
7	329	34.3	6138	6	AY036062 Arabidopsis
8	329	34.3	6138	6	ARI138346
9	328.8	34.3	6138	6	AX320930
10	322.8	33.7	1065	8	MDO251117
11	318.4	33.2	1125	6	AB025643
12	318.4	33.2	1125	6	AR003863
13	315.4	32.9	1160	8	TOBNAG1A
14	314.4	32.8	1214	8	AF265562
15	307.6	32.1	1084	8	PHPMADS3
16	296.4	30.9	1009	8	TOMTAG1A
17	295.6	30.8	1080	8	AF234617
18	295	30.8	956	8	PGORFAG2
19	293.6	30.6	1142	8	PHBPF6A
20	293.6	30.6	1197	8	AF022377
21	293.4	30.6	1224	8	AF103903
22	286.8	29.9	1201	8	PETFHP
23	285.4	29.8	1073	8	GHY9722
24	285.4	29.8	1157	6	S53900
25	285.4	29.8	1158	8	AX006357
26	285.4	29.8	1160	8	AF035438
27	281.2	29.3	1128	8	AF022379
28	280.6	29.3	1082	8	DCA271150
29	280	29.2	1054	8	AF265554
30	279.6	29.2	1097	6	AB025644
31	279.6	29.2	1098	8	AR003862
32	276	28.8	994	8	BNABAG1X
33	275.6	28.7	1000	8	GHY9723
34	275.2	28.7	1116	8	AF022378
35	275	28.7	967	8	RH043372
36	274.4	28.6	1345	8	CSCUS1
37	274	28.6	1073	8	CSA312773
38	273.4	28.5	1037	8	AB025646
39	273.2	28.5	1457	6	MDO251118
40	273.2	28.5	1458	8	AR003861
41	271.6	28.3	1048	8	ATAGMSG
42	270.6	28.2	1061	8	AF035439
43	270.4	28.2	942	8	AF099937
44	270.2	28.2	905	8	AF373604
45	270	28.2	763	8	AT020182
					AY083173 Gossypium

ALIGNMENTS

RESULT 1
ARI138348
LOCUS
DEFINITION Sequence 7 from patent US 6198024.
ACCESSION ARI138348
VERSION ARI138348.1 GI:14479857
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 959)
AUTHORS Yanofsky,M.F. and Ferrandiz,C.
TITLE Seed plants characterized by delayed seed dispersal
JOURNAL Patent: US 6198024-A 7 06-MAR-2001;
FEATURES Location/Qualifiers

QY	121	AGATAGGAGGGAAGATAGAGATAAGAGATAGAGAACACTACGAATCGTCAAGTCA	180
Db	121		
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Db	121		
QY	181	CTTCTGCAAAACGACGCAATGTTTACTCAAGAAAGCTTATGAGCTCTCTGTTGTG	240
Db	181		
QY	241	ACGCTGAGGTGCTCTGTCATCTTCTCCACTCGAGCGCTCTACGAGTACGCCACA	300
Db	241		
QY	301	ACAGTGTGAGAGGAACAATAGAAAGGTACAGAAAGCTTGCTCGAGCGCTTACCCCTC	360
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QY	361	CGACATCACCGAAGCTAATCTACTGAGTATATGAGCAAGGCGCTTAACTCCGGAG	420
Db	361		
QY	421	AGATTCGGGACATTCAGAAATTTCAACAGACACATCTTGTGATCTCTTGCTCTTGA	480
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QY	481	ACTTTAAGGAACCTCAAGAACCTTGAAGTAGGCTTGAGAAAGGATCAGTCTGTCGAT	540
Db	481		
QY	541	CCAAGAACGACGAGATGTTAGTTCGAGAGATTGAATACATGCAAAAAAGGAAATCGAG	600
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QY	601	TGCAAAACGATAACATGTATCTCCGCTCCAAGATTACTGAAAGACAGTCTACAGCAAC	660
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QY	661	AAGATTCAGTGTGATACATCAAGGACAGTTTACGAGTCGGGTGTTACTTCTCTCACC	720
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QY	721	AGTCGGGCACTATACCGGAATATATTGCGGTTTAACTTCTTGAACCGAATCAGAATT	780
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QY	841	TCCTCAGCTGAGATCGATCTATAGTGTCCACCTAAATGCGCGCGCTCCCTCAACATCTA	900
Db	841		
QY	901	GTCCCAAGCTGAGGGGAACCACTAGTGTATAGGAACCTCCCAAGAGCGGTTACACAA	959
Db	901		
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LOCUS	AY086196	1202 bp	mRNA linear
DEFINITION	Arabidopsis thaliana clone 22339		PLN 26-JUN-2002
ACCESSION	AY086196		mRNA, complete sequence.
VERSION	AY086196.1	GI:21404906	
KEYWORDS	FLI CDNA.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1202)		
REFERENCE	Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,J.L.		

TITLE	Full-length messenger RNA sequences greatly improve genome annotation		
JOURNAL REFERENCE	Genome Biol. (2002) In press		
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.		
TITLE	Full-length cDNA from Arabidopsis thaliana		
JOURNAL REFERENCE	Unpublished		
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA		
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.		
FEATURES	Location/Qualifiers		
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	322..1068		
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	/product="shatterproof 1 (SHPL)/ agamous-like 1 (AGL1)"		
	/protein_id="AAM64275.1"		
	/db_xref="GI:21592324"		
	/translation="MERGSSHDAESKLGKIEIKRIENTNROVTFCKRRNGLL KRAYELSLVCDAEVALVFSTRGRPLYEVANNVSRGTIERYKACSDANVPVSYEANTQYQOEASKLRQIRIDIONSNRHIVGSLGSLNKEKLNLEGRLEKISRVSKKNEL LVHNEYIMOKRELEQHNHMLRAKIAEGRNLNPDQOESSVIQGTTVYESGVSSHQDS QHYNNIYPVNLEPNQOFSQDQPPQLQV"		
BASE COUNT	397 a	238 c	248 g 319 t
ORIGIN			
Query Match	56.1%; Score 538; DB 8; Length 1202;		
Best Local Similarity	80.0%; Pred. No. 7.4e-146;		
Matches	664; Conservative	0; Mismatches	150; Indels 16; Gaps 2;
QY	17	CCTCACTCTCTTCTTCTTCGTGATCATTAATTAATTCGTAAGCCAGCTAGGCTTATAGA	76
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QY	77	AATGGAGGTGGTCGAGTAATGAAGTAGCAGAGCAGCAGAGAGATAGGAGAGGAA	136
Db	321	AATGGAGGAAGTGGGAGTAGTCACGCGCAGAGTAGCAAGAACTAGGAGAGGAA	380
QY	137	GATAGATAAAGAGGATAGAGAACACTAGCAATCGTCAAGTCACTTCTGCAAAACGAC	196
Db	381	AATAGAGATAAAGAGGATAGAGAACACAAATAATCGTCAAGTACTTTCTGCAAAACGAC	440
QY	197	CAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTTGTCGACCGCTGAGGTGCTCT	256
Db	441	CAATGTGCTCTCTCAAGAAAGCTTATGAACCTCTCTGTCTTGTCGATCCGAAGTTGCCCT	500
QY	257	TGTCATCTTCTCCACTCGAGCGGTCTCTACGATAGTCGCAACACAGCTGTGAGAGAAC	316
Db	501	CGTCATCTTCTCCACTCGTGGCGGTCTCTATGATAGTCGCAACACAGCTGTGAGGGGTAC	560
Y	317	AATAGAAAGGTACAAAGAAAGCTTGTCTCCGAGCGGTAAACCTCCGACCATCACCGAAGC	376

D	b	606	TGTGATACAAAGGCACGACAGTTTACGAATCCGGTGTAATCTTCATGACCAGTCGCAGCA	665
Q	y	731	GATAAACCGGAATTATATTGCGGTTAACTCTTGAACCGAATCAGAATTCCTCCCAACCA	790
D	b	666	TTATAATCGGAACATATATTCCGGTGAACCTTCTTGAACGAATCAGCAATTCCTCGGCCA	725
Q	y	791	AGACCAACCACCTCTGCAACTGTTGATTCAGTCTAAACAGCTTCTT	840
D	b	726	AGACCAACCTCTCTTCAACTTGTTGATTCAGTCTAAACAGCTTCTT	775
RESULT 5				
ARL138347				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
source				
BASE COUNT				
ORIGIN				
Query Match				
Best Local Similarity				
Matches				
DB 6; Gaps 1;				
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Q	y	137	GATGAGATATAAGAGGATAGAGAACACATPACGAATCGTCAAGTCACCTTCTGCAACGACG	196
D	b	66	AATGAGATATAAGAGGATAGAGAACACACAAATCGTCAAGTACTTCTGCAACGACG	125
Q	y	197	CATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGTCTGTGTGACGCTGAGGTGCTCT	256
D	b	126	CAATGGTCTTCTCAAGAAAGCTTATGAACTCTCTGTCTGTGTGATCGCGAATGCGCT	185
Q	y	257	TGTCATCTTCTCCACTCGAGCCGCTCTCTAGAGTACGCGCACACACAGTGTGAGGAAC	316
D	b	186	CGTCATCTTCTCCACTCGTGGCCGCTCTATGAGTACGCGCACACACAGTGTGAGGGTAC	245
Q	y	317	AATGAAAGGTACAAGAAAGCTTCTCGACGCGCTTAAACCTCCGACCATCACCAGACG	376
D	b	246	AATGAAAGGTACAAGAAAGCTTCTCGAGTCCGCTCAACCTCTCCGTCACCAGACG	305
Q	y	377	TAATACTCAGTACTATCAGCAAGAGGCGTCTAAACTCCGGAGACAGATTCGGGACATTC	436
D	b	306	TAATACTCAGTACTATCAGCAAGAGGCGTCTAAAGCTTCGGAGGACAGATTCAGATATTC	365
Q	y	437	GAATTTGAACAGACACATCTTGTGTAATCTTCTGTTCTTCTGTAATTAAGGAACCTAA	496
D	b	366	GAATTCAAATAGGCATATATTTGGGGAATCACTTGTGTTCTTGAATTCAGGAACCTAA	425
Q	y	497	GAACCTTGAAGTAGGCTTGGAGAAAGGAATCAGTCGTCTCGGATCCAAGAGCAGAGAT	556
D	b	426	AAACCTTAGAGGAGCTTCTGAAAAGGAATCAGCCGTCTCGGATCCAAGGAATGAGCT	485
Q	y	557	GTTAGTTGCAGAGATTGAATACATGCAAAAAAGGAATCAGGCTGCAAAACGATAAAT	616
D	b	486	GTTAGTGGCAGAGATAGATATATGCAAGAGAGGAAATGGAGTTGCAACACATAAAT	545
Q	y	617	GTATCTCCGCTCCAAGATTACTGAA-----AGAACAGGTTCTACGCAACAAAGATCG	670

QY	194	ACGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTCTTGTGTGAGCGCTGAGGTTC	253
Db	156	ACGCAATGGTCTTCTCAAGAAAGCTTATGAGCTCTCTGCTCTTGTGTGAGCTGGAAGTTGC	215
QY	254	TCCTGTTCATCTTCTCCACTCGAGCGCTCTCTAGAGTACGCCAACACAGTGTGAGAGG	313
Db	216	CCTCGTTATCTTCTCCACTCGTGGCTCTTATGAGTACGCCAACACAGTGTGAGAGG	275
QY	314	AACAATAGAAGGTACAGAAGCTTGTCTCGAGCGCTTAAACCTCCGACCATCACCGA	373
Db	276	TACAATTTGAAGGTACAGAAGCTTGTCTCGATGCCCTTAAACCTCTCTACTGTCACTGA	335
QY	374	AGCTAATCTCAGTACTATCAGCAAGAGCGCTCTAAACCTCCGGAGACAGATTTCGGGACAT	433
Db	336	AGCTAATACCAAGCACTATCAGCAAGAGCGCTCTAAGCTTCGGAGGAGATTCGGGACAT	395
QY	434	TCAGAATTTGAACACACATCTTGTGGTGAATCTCTTGGTTCCTTGAACCTTTAAGGAAT	493
Db	396	TCAGAATTCGAACAGGCATATTGTTGGAGAACTCACTTGGTTCATTGAACCTTCAAGGAAT	455
QY	494	CAAGAACCTTGAAGTAGGCTTGAGAAAGGAATCAGTCTGTCGGATCCAGAAACACGA	553
Db	456	CAAAAACCTTAGAAGCGCTTGAAGAAAGGAATCAGCGCGCTCCGATCCAGAAAGATGA	515
QY	554	GATCTTAGTTCAGAGATTGAATACATGCAAAAAGGAAATCGAGCTGCAAAAACGATAA	613
Db	516	ACTTTTAGTGCAGATAGAGTATATCCAGNAGGGAATGGAGTTCCAGCACGTTAA	575
QY	614	CATGTATCTCGCTCCCAAGATTACTGAA-----AGAACAGGCTTACAGCAACAAGAATC	667
Db	576	CATGTACTTAAGACTAAGATAGAACAAAGCGCGAGATTGAATCCGGAACAGCATGGATC	635
QY	668	GAGTGTGATACATCAAGGCACAGTTACAGTCCGGTGTACTTCTTC	724
Db	636	CGGTGTAATCAAGGACGGCGGTATTGAGTCCGGTCTGCTTCTTCATGATCAGTTC	695
QY	725	GGGCGAGTATACCGGAATTATATTCGGTTAACTCTTGAACCGAATCAGAAATTCCTC	784
Db	696	CGAGTATATACCGGAATTATATTCGGTTAACTCTTGAACCGAATCAACAATTCCTC	755
QY	785	CAACCAACCAACCACTCTGCAACTGTTTGA	818
Db	756	CGGTCAAGACCAACCTCTCTTCAACTTGTATA	789
RESULT 7			
ARI38346			
LOCUS	ARI38346	6138 bp	DNA linear PAT 16-JUN-2001
DEFINITION	Sequence 4 from patent US 6198024.		
ACCESSION	ARI38346		
VERSION	ARI38346.1	GI:14479855	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 6138)		
AUTHORS	Yanofsky M.F. and Ferrandiz,C.		
TITLE	Seed plants characterized by delayed seed dispersal		
JOURNAL	Patent: US 6198024-A 4 06-MAR-2001;		
FEATURES	Location/Qualifiers		
1.	.6138		
BASE COUNT	2002 a 1058 c 931 g 2147 t		
ORIGIN	/organism="unknown"		
Query Match	34.3%; Score 329; DB 6; Length 6138;		
Best Local Similarity	100.0%; Pred. No. 8.6e-85;		
Matches	329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	631	AGATTACTGAAGAAGAGGTCTACAGCAACAAGATCGAGTGTGATACATCAAGGGACAG	690
Db	5733	AGATTACTGAAGAAGAGGTCTACAGCAACAAGATCGAGTGTGATACATCAAGGGACAG	5792

QY	691	TTTACAGAGTCGGGTGTACTTCTTCTCACAGTCGGGGCAGTATAACCGGAATTATATTG	750
Db	5793	TTTACAGAGTCGGGTGTACTTCTTCTCACAGTCGGGGCAGTATAACCGGAATTATATTG	5852
QY	751	CGGTTAACCTTCTTGAACCGGAATCAGAAATTCCTCCAAACCAAGACCAACCTCTGCAAC	810
Db	5853	CGGTTAACCTTCTTGAACCGGAATCAGAAATTCCTCCAAACCAAGACCAACCTCTGCAAC	5912
QY	811	TTGTTTGAATTCAGTCTAACATAAGCTTCTTCTCAGCCTGAGATCGATCTATAGTGTC	870
Db	5913	TTGTTTGAATTCAGTCTAACATAAGCTTCTTCTCAGCCTGAGATCGATCTATAGTGTC	5972
QY	871	CCTAAATCGGGCGCGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC	930
Db	5973	CCTAAATCGGGCGCGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC	6032
QY	931	TACGAACCTCCAAAGACAGGTTTACACAAA	959
Db	6033	TACGAACCTCCAAAGACAGGTTTACACAAA	6061
RESULT 8			
AX320930			
LOCUS	AX320930	6138 bp	DNA linear PAT 14-DEC-2001
DEFINITION	Sequence 6 from Patent WO0179517.		
ACCESSION	AX320930		
VERSION	AX320930.1	GI:17902477	
KEYWORDS	thale cress.		
SOURCE	Arabidopsis thaliana		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1		
AUTHORS	Liljegren S. and Yanofsky M.F.		
TITLE	Control of fruit dehiscence in arabidopsis by indehiscent1 genes		
JOURNAL	Patent: WO 0179517-A 6 23-OCT-2001;		
FEATURES	The Regents of the University of California (US)		
1.	.6138		
BASE COUNT	2002 a 1058 c 931 g 2147 t		
ORIGIN	/db_xref="taxon:3702"		
Query Match	34.3%; Score 329; DB 6; Length 6138;		
Best Local Similarity	100.0%; Pred. No. 8.6e-85;		
Matches	329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	631	AGATTACTGAAGAAGAGGTCTACAGCAACAAGATCGAGTGTGATACATCAAGGGACAG	690
Db	5733	AGATTACTGAAGAAGAGGTCTACAGCAACAAGATCGAGTGTGATACATCAAGGGACAG	5792
QY	691	TTTACAGAGTCGGGTGTACTTCTTCTCAGCCTGAGATCGATCTATAGTGTC	750
Db	5793	TTTACAGAGTCGGGTGTACTTCTTCTCAGCCTGAGATCGATCTATAGTGTC	5852
QY	751	CGGTTAACCTTCTTGAACCGGAATCAGAAATTCCTCCAAACCAAGACCAACCTCTGCAAC	810
Db	5853	CGGTTAACCTTCTTGAACCGGAATCAGAAATTCCTCCAAACCAAGACCAACCTCTGCAAC	5912
QY	811	TTGTTTGAATTCAGTCTAACATAAGCTTCTTCTCAGCCTGAGATCGATCTATAGTGTC	870
Db	5913	TTGTTTGAATTCAGTCTAACATAAGCTTCTTCTCAGCCTGAGATCGATCTATAGTGTC	5972
QY	871	CCTAAATCGGGCGCGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC	930
Db	5973	CCTAAATCGGGCGCGCTCCCTCAACATCTAGTCGCAAGCTGAGGGGAACCACTAGTGTC	6032
QY	931	TACGAACCTCCAAAGACAGGTTTACACAAA	959
Db	6033	TACGAACCTCCAAAGACAGGTTTACACAAA	6061

BASE COUNT
ORIGIN

Query Match		33.7%;	Score 322.8;	DB 8;	Length 1065;
Best Local Similarity		68.2%;	Pred. No. 5.3e-83;		
Matches 479;		Conservative	0;	Mismatches 217;	Indels 6; Gaps 2;
QY	117	AAGAAGATAGGAGAGGAGAGATAGAGATAAAGAGGATAGAGAACACTACGAAATCGTCAA	176		
DB	55	AAGAAATTTGGAGAGGAGAAATCGAGATCAAGAGGATCGAAACACTACCAATCGACAA	114		
QY	177	GTCACTTTTCGCAACAGCAGCAATGGTTTACTCAAGAAGCTTATGAGCTCTCTGCTTTG	236		
DB	115	GTCACTTTTCGCAACAGCAGCAGGTTTGGTTTAAAGACATATGAACATATCTGTTCTT	174		
QY	237	TGTGACGCTGAGGTTGCTTCTTGTTCATCTTCCACTCGAGCGCGTCTTACGAGTACGCC	296		
DB	175	TGTGATGCTGAAGTTGCTTCTTATTTGTTCTCTACCCGGGGCGCTCTATGAATATGCT	234		
QY	297	AACAACAGTGTGAGAGGAACAATAAGAAAGGTACAAAGAGCTTGTCTCCGAGCGCGTTAAC	356		
DB	235	AACAACAGTGTGAGAGGAACAATAAGAAAGGTACAAAGAGCATG---TGATTTCTCAAAAC	291		
QY	357	CCTCCGACCATCACCGAAGCTAATCTACGTACTATCAGCAAGAGGCGTCTAAACTCCGG	416		
DB	292	ACTGGATCTGTAACTGAGACTTAATGTTCAAGTTTATCAGCAAGAGGCGCTCCAAACTAAGA	351		
QY	417	AGACAGATTCGGGACATTCAGAATTTGAACAGACACATCTTGTGTAATCTCTTGGTTCC	476		
DB	352	AGACAGATTAAGAGAAATTCAGAATTCAAACAGGCACATCTAGGTGAAGCTCTTAGCACT	411		
QY	477	TTGAACCTTTAAGGAACCTCAAGAACTTGAAGAGTGGGTTGAGAAAGGAATCAGTCTGTC	536		
DB	412	TTGAACCTCAAGGAACCTCAAGAACTTGAAGAGTGGGTTGAGAAAGGAATCAGCAGAATA	471		
QY	537	CGATCCAAAGACGAGAGATGTTAGTTCAGAGATTGAATACATCAAAAGAGGAAATC	596		
DB	472	AGATCCAAAGAGATGAATGCTGTTGCTGAATTCGAATATATCGAAGAGGAGATC	531		
QY	597	GAGCTGCAAAACGATAACATGTATCCGCTCCAAAGATTACTGAAAGACAGGTTCTACAG	656		
DB	532	GAGCTGCAAAATCATAACAATTTCTGAGAGCAAGATTGCTGAAATGACAGGGGCACAA	591		
QY	657	CAACAAGATCAGTGTGATACATCAAGGGACAGTTTAGGAGTCGGGTGTTACTTCTTCT	716		
DB	592	CAGCAGCAAGCAAAATATGAT---GCCAGGAACATTTATCTGCGTATGATCAATCAATGCCT	648		
QY	717	CACCAGTCGGGCGATGAACGGGAATATATGCGGTTTAACCTTCTTGAACCGGAATCAG	776		
DB	649	CCTCCTCAATCATGATAGGAGCTTCTCCCTGTAAATCCITGAGTCCCAATCACCCTAC	708		
QY	777	AATTCTCTCAACCAAGACCAACCACTCTGCAACTTGTGTA	818		
DB	709	AATGCCAAGGCGACAGACACACTCTCCAACCTGTTTGA	750		

RESULT 11	AR003863	LOCUS	AR003863	Sequence 6 from patent US 5744693.	DNA	linear	PAT 04-DEC-1998
DEFINITION	AR003863	ACCESSION	AR003863.1	GI:3965122			
VERSION	Unknown.	KEYWORDS	Unknown.				
SOURCE	Unknown.	ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1125)						
AUTHORS	Meyerowitz,E.M., Yanofsky,M.F. and Ma,H.						
TITLE	Plants having altered floral development						
JOURNAL	Patent: US 5744693-A 6 28-APR-1998;						
FEATURES	Location/Qualifiers						
source	1. 1125						
BASE COUNT	377 a 216 c 222 g 310 t						
ORIGIN							

Query Match		33.2%;	Score 318.4;	DB 6;	Length 1125;
Best Local Similarity		65.8%;	Pred. No. 1e-81;		
Matches 479;		Conservative	0;	Mismatches 246;	Indels 3; Gaps
QY	117	AAGAAGATAGGAGAGGAGGAGATAGAGATAAAGAGAGGATAGAGAACACTACGAAATCGTCAA	176		
Db	152	AGGAAACTGGGAAGAGGAAGATTGAGATCAAAACGGATGAAACACAGCAAGCAATCGTCAA	211		
QY	177	GTCACTTTCTGCAAAAGCAGCGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTGG	236		
Db	212	GTCACTTTCTGCAAGAGAGCGCAATGGTTTACTCAAAAGGCGCTATGAATATCTGTGCTC	271		
QY	237	TGTGACGCTGAGGTTGCTCTTGTTCATCTTCTCCACTCGAGGCGGCTCTACGAGTACGCC	296		
Db	272	TGTGATGCTGAGGTTGCTTGTGATTGTTCTTCAAGCAGAGGCGAGACTCTATGAGTATGCC	331		
QY	297	ACAACAGTGTGAGAGGAACAATAGAAAGGTACAAAGAAAGCTTGTCCGACGCCGTTAAC	356		
Db	332	AACAACAGTGTGAAGACCAAAATTGAGAGGTTACAAAGAAAGCTTGTTCAGATTCTCTCAAC	391		
QY	357	CCTCCGACCATCACCGAAGCTAATCTACGTACTATCAGCAAGAGGCGCTTAAACTCCCG	416		
Db	392	ACTGGTTCAATTTCCGAGGCGCAATGCTCAGTATTATCAGCAAGAGGCTCCAAACTCGCG	451		
QY	417	AGACAGATTCGGGACATTCAGAATTTGAACAGACACATCTTGGTGAATCTCTTGGTTCC	476		
Db	452	GCACAAATTTGGAATCTGCAGAAATCAGAACAGGAACATGTTGGTGAATCACTGGCTGCA	511		
QY	477	TTCAACTCTTAAAGGAACCTCAAGAACTTGAAGTAGGCTTGAGAAAGGAATCAGTCTGTC	536		
Db	512	CTGAGCTCTAGAGATCTGAAGAATCTGGAACAAAAATTTGAAAAGGCTATTGCAAAATC	571		
QY	537	CGATCCAAAGAACGACGAGATGTTAGTTGACAGATTGAATACATCAAAAGGGAATC	596		
Db	572	AGATCCAAAGAAATGAGCTGCTGTTTGGTGAATTCAGTACATCGAAGAGGGAAT	631		
QY	597	GAGCTGCAAAACGATACATGTATCTCCGCTCCCAAGATTACTGAAA---GAACAGGTCTA	653		
Db	632	GATTTACACAAACAATCATCAGTCTGAGAGCAAAAGATTGCTGAACTGAGAGAGCTCAG	691		
QY	654	CAGCAACAAGAAATCGAGTGTGATACATCAAGGGACAGTTTACGAGTCGGTGTACTTCT	713		
Db	692	CAGCAGCAGCAGCAGCAGATGAACCTTGATGCCAGGAGTTTCAAGCTATGAGCTTGTG	751		
QY	714	TCATCACCAGTCGGGCGAGTATACCCGGAATTTATATTCGGTTTAACTTCTTGAACCGAAT	773		
Db	752	CTCCACCTCATCAATTTGATACCTCGAAACTATTTACAAGTTAATGGTTTGCAACCAAC	811		
QY	834	GCTTCTTT 841			
Db	872	TCTATGTT 879			
RESULT 12					
TOBNAG1A					
LOCUS	TOBNAG1A	1125 bp	mRNA	linear	PLN 29-MAR-1994
DEFINITION	Nicotiana tabacum	NAG1 mRNA, complete cds.			
ACCESSION	L23925				
VERSION	L23925.1	GI:431735			
KEYWORDS	.				
SOURCE	Nicotiana tabacum cDNA to mRNA.				
ORGANISM	Nicotiana tabacum				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.					
REFERENCE	1 (bases 1 to 1125)				
AUTHORS	Kempin,S.A., Mandel,M.A. and Yanofsky,M.F.				
TITLE	Conversion of perianth into reproductive organs by ectopic				

expression of the tobacco floral homeotic gene NAG1
Plant Physiol. 103 (4), 1041-1046 (1993)
94120000
PUBMED
7507255

FEATURES

Location/Qualifiers

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CDS

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/note="MADS-box"

/function="DNA binding domain"

377 a 216 c 222 g 310 t

BASE COUNT

ORIGIN

Query Match 33.2%; Score 318.4; DB 8; Length 1125;
Best Local Similarity 65.8%; Pred. No. 1e-81;
Matches 479; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

QY 117 AAGAAGATAGGAGGAGGAGATAGAGATAAGAGATAGAGACACTAGCAATCGTCAA 176

Db 152 AGAAACTGGGAAGGAAGGAAGTGGAGTCAACACGATCGAACAACACGAATCGTCAA 211

QY 177 GTCACATTCTGCAACAGCGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTG 236

Db 212 GTCACATTCTGCAACAGCGCAATGGTTTACTCAAGAAAGCTTATGAGCTCTCTGCTTG 271

QY 237 TGTGAGCTGAGGTGCTCTTCTCACTCTTCTCACTGAGGCGCTCTACGAGTACGCC 296

Db 272 TGTGATGCTGAGGTGCTTGTGATGCTTCTCAAGCAGAGCGACGCTATGAGTATGCC 331

QY 297 AACACAGTGTGAGAGCAACAATGAAAGGTACAGAAAGCTTGCTCCGACGCGTTAAC 356

Db 332 AACACAGTGTGAGAGCAACAATGAGAGGTACAGAAAGCTTGTTCAGATTCCTCAAAC 391

QY 357 CCTCCGACCATCAGCAAGCTAATCTACTAGTACTATCAGCAAGAGCGCTTAAACTCCGG 416

Db 392 ACTGGTTCAATTCGAGGCCAATGCTAGTATATCAGCAAGAGCGCTTAAACTCCGG 451

QY 417 AGACAGATTCGGACATTCAGAAATTTGACACACACATCTTGGTGAATCTCTGGTTCC 476

Db 452 GCACAAATTTGAAATCTCGAATTCAGACAGCAAGCAATCTGGGTGAATCACTGGCTGCA 511

QY 477 TTGAACCTTTAAGGAACCTCAAGAACCTTGAAGCTAGGCTTGAGAAAGGAATCAGTCGTC 536

Db 512 CTGAGCCTCAGAGTCTGAGAAATCTGGACAAAATTTGAAAAGGCATTAAGCAAAATC 571

QY 537 CGATCCAAAGACGACGATGTTAGTTGTCAGAGATTTGAATATGCAAAAAGGGAATC 596

Db 572 AGATCCAAAAGAAATGAGCTGCTGTTTGTGTAATTTAGTACATGACAGAGAGGAAAT 631

QY 597 GAGTGTCAAAACGATAACATGTATCTCCGCTCCAGATTTACTGAAA---GAACAGGTCTA 653

Db 632 GATTTCACAAACAATCAGTACCTGAGAGCAAGAAATGCTGAAAACCTGAGAGAGCTCAG 691

QY 654 CAGCAACAAGAAATCGAGTGTGATACATCAAGGACAGTTTACGAGTCGGGTGTTACTTCT 713

Db 692 CAGCAGCAGCAGCAGCAGATGAACTTGATGCCAGGAGTTCAAGCTATGAGCTGTG 751

QY 714 TCTCACCAGTCGGGCGAGTATAACCGGAATATATATTGCGGTTAACCTTCTTGAACCGAAT 773
Db 752 CTCCACCTCATCAATTTGATGACTCGAAACATATTTACAAGTTTAATGGTTTGCACCAAC 811
QY 774 CAGAATTCCTCCAAACCAAGACCACTCTGCAACCTTGTGTTGATTCAGTCTTAACATAA 833
Db 812 AACCATTTACACTAGACAGACCACTCTCTTCAACTAGTCTAATATGTTGTTGAAAGTCT 871
QY 834 GCTTCTTT 841
Db 872 TCTATGTT 879

RESULT 13

AF265562

LOCUS

DEFINITION

cds.

ACCESSION

AF265562

VERSION

AF265562.1

KEYWORDS

SOURCE

ORGANISM

Vitis vinifera.

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;

Vitaceae; Vitis.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

1;

32.9%;

Score 315.4;

DB 8;

Length 1160;

Pred. No. 7.7e-81;

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18;

311 t

QY	240	GAGCGTGAAGTGGCTCTGTCTGTCTCATCTCTCCACTCGAGCGCGTCTCTACGAGTACGCCAAC	299
Db	317	GATGCAGAAAGTGTCTCATCTCTCTCCAGCGCTGGCGGCTCTATCAATATGCTAAC	376
QY	300	AACAGTGTGAGAGGAACAATAAGAGGTACAGAAGCTTGTCTCCAGCGCGGTAAACCCCT	359
Db	377	AACAGTGTGAGAGGAACAATAAGAGGTACAAAAAGTGTGTCTGATTCCTCCCAATACC	436
QY	360	CCGACCATACCGAAGCTAATACACTCAGTACTATCATCAGCAAGAGCGCTCTAAACTCCGGAGA	419
Db	437	GGATCTCTTCTGAAGCTAATGCTCAGTCTTTACCGAAGAGCGCTCCAAAATGCGCCCGT	496
QY	420	CAGATTCGGGACATTCAGAAATTTGAACAGACACATCTTGTGGAATCTCTTGGTTCCTTG	479
Db	497	CAATCAGGATATACAGAAATTTGNACAGGATATTTCTGGGTGAGGCTCTTAGCTCTCTG	556
QY	480	AACTTTAAAGAACTCAAGAACTTTGAAAGTGGCTTGAAGAAAGGAATAGTCGTGTCCGA	539
Db	557	AACTTTAAAGAACTCAAGAACTCTGGAGACCAGGCTGGAGAAAGGTATCAGCAGAATCAGA	616
QY	540	TCCAAGAGCAGAGATGTTAGTTCCAGAGATTGAATACATCGAAAAAGGGAATCGAG	599
Db	617	TCCAAAAAGAAATGAATGCTGTTGCTGAAATCGAGTACATCAAAAAGGAGAGATTGAG	676
QY	600	CTGCAAAACGATAACATGTATCTCCGCTCCAAGATTACTGTAAGAACACAGGTCTTACAGCAA	659
Db	677	CTCAAAACAGTAACATTTCTCGAGCACAGATAGCTGAGAAATGAGAGAGGCCCAACAG	736
QY	660	CAGAATCGAGTGTATACATCAAGGGACAGTTTAGAGTCGGGTACTTCTTCTTCAC	719
Db	737	CAATGAACCTGATGCCAGGGTCTCAGTACGAGAGCGTCCG-----	778
QY	720	CAGTCGGGCGAGTAAACCGGAATATATTTGCGGTTAACTTCTTGAACCGGAATCAGAAT	779
Db	779	CAGCAGCATACGACTCTCAAACTTGCTCCCTGTGTAACTCTCTGACCCCTAATACCAT	838
QY	780	TCCTCCAAACCAAGACCAACCACTCTCGCAACTGTTTGA	818
Db	839	TACTCTCGCCACGCAACACAGCTCTCCAACACTAGTGTGA	877
RESULT 14			
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LOCUS			
DEFINITION			
P.hybrida pMADS3 mRNA.			
ACCESSION			
X72912			
VERSION			
X72912.1 GI:313112			
KEYWORDS			
homeotic flower gene; MADS box; pMADS3 gene; transcriptional regulation.			
SOURCE			
ORGANISM			
Petunia x hybrida.			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.			
REFERENCE			
AUTHORS			
Tsuchimoto,S., van der Krol,A.R. and Chua,N.H.			
TITLE			
Ectopic expression of pMADS3 in transgenic petunia phenocopies the petunia blind mutant			
JOURNAL			
Plant Cell 5 (8), 843-853 (1993)			
MEDLINE			
94004017			
PUBMED			
8104573			
REFERENCE			
2 (bases 1 to 1214)			
Tsuchimoto,S.			
AUTHORS			
Direct Submission			
TITLE			
Submitted (26-MAR-1993) S. Tsuchimoto, The Rockefeller University, 1230 York Ave., New York, NY 10021, USA			
JOURNAL			
Location/Qualifiers			
1. .1214			
FEATURES			
source			
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Best Local Similarity	66.7%;	Pred. No. 1.5e-80;		
Matches 472;	Conservative	0;	Mismatches 221;	Indels 15;
Gaps	1;			
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Db	201	AGGAAACTAGGAAGAGGAAAGATTGAGATCAAGAGATCGAAAAACACGACAAATCGCAA	260	
QY	177	GTCAGTTTCTGAAAACGAGCGCAATGCTTTACTCAAGAAAGCTTATGAGTCTCTGTCTTG	236	
Db	261	GTCAGTTTGTGACAGAGCGCAATGCTTGTCTCAAAAAGCCCTATGAATATCTGTGCTC	320	
QY	237	TGTGACGCTGAGTGTGCTTGTTCATCTTCTCCACTCGAGGCGCTCTACGAGTAGCGCC	296	
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QY	297	AACAACAGTGTGAGAGGAACAATAGAAAGGTACAGAAAGCTTCTCGAGCGCGTTAAC	356	
Db	381	AACAACAGTGTGAAAGCAACAATTTGAGAGGTACAGAAAGCTTGTTCAGATTTCTCAAAC	440	
QY	357	CCTCCGCCATCAGCAAGCTAATACTACTACTATCAGCAAGAGGCGTCTTAAACTCCGG	416	
Db	441	ACTGTTTCAATTTGCCGAAGCTATGCTCAGTATACCAGCAAGAGCTCCAACCTCGT	500	
QY	417	AGACAGATTCGGGACATTCAGAAATTTGAACAGACACATTTCTTGTGTAATCTCTTGGTTCC	476	
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QY	537	CGATCCAAAGACACAGAGATGTTAGTTGCAGAGATTGAATACATGCAAAAAAGGAAATC	596	
Db	621	CGAGCCAAAAGAAAGAGCTGTTGTTGCTGAAATTCAGTATATGCAAAAGAGGAAAT	680	
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QY	657	CAACAAGAACTCAGTGTGTATACATCAAGGACAGTTTTACGAGTCGGGTGTTACTTCTCT	716	
Db	741	CA-----GATGAACCTTGATGCCCTGGGAGTCTAGCTATGACCTGTGCGCT	785	
QY	717	CACCAAGTCGGGCGAGTATAACCGGAATATATTGCGGTTAACTTCTTGAACCGGAATCAG	776	
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Db	846	CATTACCTAGACAAGACCAACCACTCTTCAACTAGTCTAAATTTATT	893	

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DEFINITION    Lycopersicon esculentum TAG1 mRNA, complete cds.
ACCESSION     L26295
VERSION       L26295.1 GI:457381
KEYWORDS
SOURCE
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ORGANISM      Lycopersicon esculentum
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               pistil cDNA library in lambda gt10 from C. Gasser) mature pistils
               cDNA to mRNA.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE     1 (bases 1 to 1084)
AUTHORS      Pnueli,L., Hareven,D., Rounsley,S.D., Yanofsky,M.F. and
               Lifschitz,E.
TITLE         Isolation of the tomato AGAMOUS gene TAG1 and analysis of its
               homeotic role in transgenic plants
JOURNAL       Plant Cell 6 (2), 163-173 (1994)
MEDLINE       94198593
PUBMED        7908549
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Best Local Similarity 65.7%; Pred. No. 1.5e-78;
Matches 464; Conservative 0; Mismatches 239; Indels 3; Gaps 1;
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Db 171 GTAACATCTGCAAGAGGCGCAATGTTTGTCTTAAAGGCGCTTATGAATGTGTGCTC 230
Qy 237 TGTGAGCGTGTGAGTGTCTGTTCATCTTCTCCACTCGAGGCGCTCTCTACGAGTACGCC 296
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